

```

ID AAF75831 standard; DNA; 20 BP.
AC AAF75831;
XX
XX
DT 22-OCT-2001 (first entry)
XX
XX Human C2 domains protein, BioHC2, coding sequence PCR primer #2.
DE
XX Human; C2 domain protein; BioHC2; membrane protein; PCR primer;
KW transmembrane transport disorder; ss.
XX
XX Homo sapiens.
OS
XX CN1296954-A.
DN
XX 30-MAY-2001.
PD
XX
XX 19-NOV-1999; 99CN-00124028.
PF
XX 19-NOV-1999; 99CN-00124028.
PR
XX (SHEN-) SHENGYUAN GENE DEV CO LTD SHANGHAI.
PA
XX Mao Y, Xie Y;
PI
XX WPI; 2001-489555/54.
DR
XX Human membrane protein containing C2 structural domain and its coding
PT sequence.
PT
XX Example 3; Page 12 (Disclosure); 26pp; Chinese.
PS
XX The present invention relates to human C2 domains protein, BioHC2 and
CC coding sequence (see AAF75829 and AAG56417). BioHC2 is a membrane
CC protein, which contains C2 structural domains. BioHC2 and its coding
CC sequence are useful for treating transmembrane transport disorders. The
CC present sequence is a PCR primer, which was used in an example from the
CC present invention
XX
XX Sequence 20 BP; 5 A; 1 C; 4 G; 10 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AAAGATTATTTT 435
DB 5 AAAGATTATTTT 16

RESULT 269
AAF23187
ID AAF23187 standard; DNA; 20 BP.
XX
XX AAF23187;
AC
XX
XX 19-MAR-2001 (first entry)
DT
XX
DE Oligonucleotide for detection of Mycobacterium vaccae.
XX
XX ITS; internal transcribed spacer region; Mycobacterium fortuitum;
KW Mycobacterium chelonae; Mycobacterium abscessus; Mycobacterium vaccae;
KW Mycobacterium flavesens; Mycobacterium asiaticum; tuberculosis;
KW Mycobacterium porcinum; Mycobacterium acapulcensis; identification;
KW Mycobacterium diernhoferi; PCR primer; probe; detection; ss.
XX
XX Mycobacterium vaccae.
OS
XX
XX WO200073436-A1.
PN
XX
XX 07-DEC-2000.
PD
XX
XX 16-MAY-2000; 2000WO-KR000477.
PF

XX 29-MAY-1999; 99KR-00019631.
PR 29-MAY-1999; 99KR-00019632.
PR 29-MAY-1999; 99KR-00019633.
PR 29-MAY-1999; 99KR-00019634.
PR 29-MAY-1999; 99KR-00019635.
PR 07-APR-2000; 2000KR-00018189.
XX
XX (SJHI-) SJ HIGHTECH CO LTD.
PA (KIMC/) KIM C M.
PA (PARK/) PARK H K.
XX
XX Kim CM, Park HK, Jang HJ;
PI
XX WPI; 2001-061527/07.
DR
XX
XX Novel oligonucleotide sequences of internal transcribing spacer region of
PT non-tuberculosis mycobacteria (NTM) used as probes or primers for
PT detecting and identifying mycobacteria and distinguish TB complex from
PT NTM.
XX
XX Claim 16; Page 45; 89pp; English.
PS
XX The present sequence is an oligonucleotide developed using a
XX Mycobacterium ITS (internal transcribed spacer region) nucleotide
CC sequence. ITS DNA sequences from M. fortuitum, M. chelonae, M. abscessus,
CC M. vaccae, M. flavesens, M. asiaticum, M. porcinum, M. acapulcensis, M.
CC diernhoferi genes were identified. The oligonucleotides derived from
CC these sequences were used to develop PCR primers and hybridization probes
CC for detection and identification of Mycobacterium. ITS has a more
CC polymorphic region than 16S rRNA and also has a conserved region. It is
CC therefore highly effective as a target DNA for distinction of genotype.
CC The oligonucleotide probes, attached to solid substrate, hybridise only
CC with nucleotide sequences in ITS of specific mycobacteria, and thus they
CC can detect and identify the specific mycobacteria sensitively. The
CC oligonucleotides can also detect and identify the specific mycobacteria
CC by PCR amplification. Using the oligonucleotide primers or probes made
CC from ITS of mycobacteria, it is possible to detect mycobacteria,
CC distinguish tuberculosis (TB) complex from non-tuberculosis mycobacteria
CC (NTM), and to identify mycobacteria species accurately and effectively
XX
XX Sequence 20 BP; 1 A; 3 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGGTCGGCGTG 76
DB 5 AGGGTCGGCGTG 16

RESULT 270
AAS22314
ID AAS22314 standard; DNA; 20 BP.
XX
XX AAS22314;
AC
XX
XX 24-OCT-2001 (first entry)
DT
XX
XX Human COL9A2 PCR primer 1 for Exon 17.
DE
XX
XX Human; collagen; COL1A1; COL1A2; COL9A1; COL9A2; COL9A3; ss;
KW osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;
KW shortness of stature; low bone density; gene therapy; PCR primer.
XX
XX Homo sapiens.
OS
XX
XX US6265157-B1.
PN
XX
XX 24-JUL-2001.
PD
XX
XX 03-OCT-1997; 97US-00943731.
PF

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XX 03-DEC-1991; 91US-00803628.
PR 13-MAR-1994; 94US-00212322.
XX
XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (UYOU-) UNIV OULU.
XX
PR Prockop DJ, Spotila LD, Deltas CD, Sereda L;
PI Westerhausen Larson A, Pack M, Collige A, Early J, Koerkkoe J;
PI Ala-Kokko L, Annunen S, Pihlajamaa T, Vuoristo M, Paasilta P;
XX WPI; 2001-432201/46.
DR
XX
XX Detecting collagen gene alteration, useful for diagnosing osteoporosis,
PT multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of
PT stature and low bone density in humans.
XX
XX Claim 8; Fig 24; 617pp; English.
XX
XX The invention relates to detecting a collagen gene alteration associated
CC with a pathological condition in a human subject by obtaining from the
CC subject a sample nucleic acid containing a portion of at least 15
CC consecutive nucleotides of the segment of the COL1A1 gene extending in
CC the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent
CC exon 28 through the 3' end of intron 51, where the portion contains an
CC intronic nucleotide and a first and second site, determining the sequence
CC of the portion and comparing the sequence of the portion with the
CC corresponding consensus sequence of the COL1A1 gene where a difference
CC between the sequence of the portion and the consensus sequence indicates
CC the presence of the collagen alteration in the subject. The method is
CC used for detecting abnormalities in a COL1 or COL9 gene is useful for
CC determining whether a subject is afflicted with pathological conditions
CC associated with an altered collagen gene such as osteoporosis, multiple
CC epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and
CC low bone density. Identification of an abnormality in a collagen gene is
CC also useful for designing a therapeutic nucleotide or gene therapy agent
CC which can be administered to the subject to correct or alleviate the
CC abnormality. The method is useful for detecting mutations in both the
CC coding and non-coding sequences of any of the COL1 or COL9 genes.
CC Therefore the method can be used to detect collagen gene alterations
CC which affect either the primary sequence of a collagen protein chain,
CC splicing of the mRNA encoding such chains or regulation of expression of
CC the genes encoding such chains. The present sequence is a PCR primer
CC which amplifies a nucleic acid from a collagen gene of the invention
XX
XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CTGGGACCTTAGA 212
Db |||||
3 CTGGGACCTTAGA 14

RESULT 271
ABA94350
ID ABA94350 standard; DNA; 20 BP.
XX
XX ABA94350;
AC
XX
XX 26-MAR-2002 (first entry)
DT
DE Beta-actin gene fragment amplifying primer Beta ACT-2.
XX
XX Immunostimulant; circularity; angiogenesis; xenotransplantation;
KW metabolic; cytostatic; vulnary; implant; cell growth promoter;
KW JHF gene; beta-actin; PCR primer; ss.
XX
XX Synthetic.
OS
XX

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PN WO200185917-A2.
XX
XX 15-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-GB002056.
XX
XX 10-MAY-2000; 2000US-00568254.
PR 18-JAN-2001; 2001GB-00001315.
PR 26-FEB-2001; 2001US-0271497P.
PR 21-MAR-2001; 2001GB-00007093.
XX
XX (TRIS-) TRISTEM IRELAND LTD.
PA
XX
XX Abuljadayel IMS;
FI
XX WPI; 2002-114181/15.
DR
XX
XX New device for forming and/or increasing the relative number of
PT undifferentiated cells in a cell population (e.g. hematopoietic cells)
PT and for manufacturing a medicament for treating an immunological
PT disorders or cancers.
XX
XX Disclosure; Page 67; 169pp; English.
XX
XX The invention relates to a device for forming and/or increasing the
CC relative number of undifferentiated cells in a cell population including
CC committed cells. The device comprises a means for contacting a more
CC committed cell with a retrodifferentiation means or an agent that causes
CC the more committed cell to retrodifferentiate into an undifferentiated
CC cell. The device is particularly useful for forming and/or increasing the
CC relative number of (a) undifferentiated cells in a cell population
CC including hematopoietic cells; (b) cells having a cell surface marker
CC designation CD34+ and/or HLA-DR+ and/or CD38+ and/or CD117 and/or
CC AC133 and/or CD90 and/or CD45low in a cell population. The
CC retrodifferentiating means of the device is useful for displacing the
CC ratio of normal differentiated cells in a cell population to effect
CC retrodifferentiation of one or more of the differentiated cells to an
CC undifferentiated cell(s). The device and the recommitted cells may be
CC used to manufacture a medicament for treating an immunological disorder
CC or disease. The medicament is useful for treating cancer, autoimmune
CC diseases, blood disorders, cellular or tissue regeneration, organ
CC regeneration, organ or tissue transplants, or congenital metabolic
CC disorders. In particular, device for preparing a stem cell from a more
CC differentiated cell. The stem cells produced are used to repopulate
CC specific cell populations in a patient, such as a haematopoietic cell
CC population or a subpopulation of it, such as CD4 T-lymphocytes and may
CC also be used to heal and reconstitute specialized cell tissue and organs.
CC Sequences ABA94349-350 represents PCR primers for amplifying a fragment
CC of the beta-actin gene
XX
XX Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
Db |||||
5 TGAGGATCTTCA 16

RESULT 272
ABK52018
ID ABK52018 standard; DNA; 20 BP.
XX
XX AC
XX ABR52018;
XX
XX 13-AUG-2002 (first entry)
DT
XX Lambda g11 insert PCR primer Fil.
XX
XX cDNA library; cloning; human disease gene; plant; animal; primer;
KW identification; food production; lambda g11 insert; PCR; ss.
XX

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XX OS Bacteriophage lambda.
XX FN US6372436-B1.
XX PD 16-APR-2002.
XX PF 14-SEP-2000; 2000US-00662235.
XX PR 14-SEP-2000; 2000US-00662235.
XX PA (UMOR ) UNIV MISSOURI.
XX PI Pouzyrev AT, Riddle DL;
XX DR WPI; 2002-433676/46.
XX PT Producing a cDNA library enriched for rare cDNAs and reduced in abundant
XX PT cDNAs to accelerate the identification and cloning of human disease
XX PS genes.
XX PS Claim 14; Col 32; 24pp; English.
XX CC The present invention relates to a new method of producing a cDNA library
XX CC enriched for rare cDNAs and reduced in abundant cDNAs. The method of the
XX CC invention is useful for providing an abundant cDNA pool to create a cDNA
XX CC library with increased representation of rare clones which may expedite
XX CC the identification and cloning of human disease genes. The invention is
XX CC also useful in the cloning of plant or animal genes of importance to food
XX CC production. The method is simple and eliminates steps for in vitro
XX CC transcription and avoids the use of quenching oligonucleotides to prevent
XX CC hybridisation between common sequences in the vector. The present nucleic
XX CC acid sequence represents lambda gt11 insert PCR primer F11 that was used
XX CC in the methods of the invention for library construction and phage DNA
XX CC preparation
XX SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

QY 246 CTCCTGGAGCCC 257
DB 1 CTCCTGGAGCCC 12

RESULT 273
ABN79607/C
ID ABN79607 standard; DNA; 20 BP.
XX AC ABN79607;
XX DT 29-JUL-2002 (first entry)
XX DE Human Fas chimeric phosphorothioate oligonucleotide #19.
XX KW Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic;
XX KW vasotropic; hepatitis; cancer; allograft rejection; ds; Fas.
XX OS Homo sapiens.
XX PN US2002004490-A1.
XX PD 10-JAN-2002.
XX PF 09-MAR-2001; 2001US-00802669.
XX PR 12-APR-1999; 99US-00290640.
XX PR 18-SEP-2000; 2000US-00665615.
XX PA (DEAN/) DEAN N M.
XX PA (MARC/) MARCUSON E G.

(WYAT/) WYATT J.
(ZHAN/) ZHANG H.
Dean NM, Marcusson EG, Wyatt J, Zhang H;
WPI; 2002-204886/26.
Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand,
Fas ligand or Fas associated protein-1 is useful for inhibiting expression of
Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating
hepatitis.
Claim 3; Page 13; 84pp; English.
This invention relates to an antisense compound encoding Fas, Fas ligand,
or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated
signalling is thought to be immunosuppressive, antiinflammatory,
hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were
designed to target human Fas. Oligonucleotides were synthesised as
chimeric oligonucleotides and are useful for treating an animal having an
autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition
associated with apoptosis, allograft rejection, or ischemia reperfusion
injury. Optionally, the above mentioned conditions are prevented by
contacting the allograft with the antisense oligonucleotide. The
oligonucleotides are used in diagnostics, therapeutics, prophylaxis and
as research reagents and in kits. The oligonucleotides are also useful
for research purposes. The present nucleotide sequence is related to
human Fas
SQ Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

QY 171 GGAATTGCTCTT 182
DB 20 GGAATTGCTCTT 9

RESULT 274
ABL43643/C
ID ABL43643 standard; DNA; 20 BP.
XX AC ABL43643;
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:687.
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2001321190-A.
XX PD 20-NOV-2001.
XX PF 12-MAR-2001; 2001JP-00068285.
XX PR 10-MAR-2000; 2000JP-00066716.
XX PA (RIKA ) RIKAGAKU KENKYUSHO.
XX PA (GENO-) GENOTEX YG.
XX DR WPI; 2002-144136/19.
XX PT Arraying genome clones.
XX PS Claim 4; Page 18; 528pp; Japanese.
XX CC The present invention describes a method of arraying genome clones. The

```

method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCTGTG 349
| | | | | | | | | |
Db 12 TCTACTTCTGTG 1

RESULT 275
ABL44379
ID ABL44379 standard; DNA; 20 BP.
XX AC ABL44379;
XX 11-APR-2002 (first entry)
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1423.
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX Homo sapiens.
XX JP2001321190-A.
XX 20-NOV-2001.
XX 12-MAR-2001; 2001JP-00068285.
XX 10-MAR-2000; 2000JP-00066716.
XX (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX WPI; 2002-144136/19.
XX Arraying genome clones.
XX Claim 4; Page 32; 528pp; Japanese.
The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to

the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 TGCATGAAATTT 505
| | | | | | | | | |
Db 8 TGCATGAAATTT 19

RESULT 276
AAL47225
ID AAL47225 standard; DNA; 20 BP.
XX AC AAL47225;
XX 22-AUG-2002 (first entry)
XX Single-stranded nucleic acid synthesis method related outer primer #3.
XX Single-stranded nucleic acid synthesis; strand displacement polymerase;
XX restriction site; probe; hybridisation assay; PCR; primer; ss.
XX Unidentified.
XX WO200234907-A1.
XX 02-MAY-2002.
XX 26-OCT-2001; 2001WO-JP009452.
XX 27-OCT-2000; 2000JP-00328219.
XX (EIKE) EIKEN KAGAKU KK.
XX Nagamine K, Hase T, Notomi T;
XX WPI; 2002-417131/44.
XX Synthesizing one of the sense and antisense strands of double-stranded nucleic acid by cleaving recognition sites in the 5' side, annealing single-stranded regions of DNA before synthesis from 3'-end of the primer.
XX Example 6; Page 47; 50pp; Japanese.
The present invention relates to a method for synthesising a single-stranded nucleic acid, involving cleaving a double-stranded DNA having a restriction enzyme recognition sequence in the 5' side of a target sequence, annealing and synthesis of a nucleic acid starting from the 3'-end of the primer with a strand displacement polymerase. The method is applicable in the selective synthesis of a single-stranded nucleic acid, particularly one of the sense and antisense strands of double-stranded nucleic acid, for use as e.g. probes for hybridisation assay. The present invention is a PCR primer described in the exemplification of the

Sequence 20 BP; 8 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCCAC 330
 |||||
 DB 7 AGGATCTTCCAC 18

RESULT 277
 ABK14334
 ID ABK14334 standard; DNA; 20 BP.
 AC
 AC ABK14334;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human interleukin-2 antisense PCR primer.
 XX
 KW Human; ss; PCR; primer; interleukin-2; neuroprotective; nootropic;
 KW anticonvulsant; cerebroprotective; antiparkinsonian; vulnerary;
 KW immunosuppressive; microglia cell line; autoimmune disease;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; amyotrophic lateral sclerosis; stroke;
 KW spinal cord injury; ataxia; brain trauma; multiple sclerosis;
 KW acquired immunodeficiency syndrome; AIDS-dementia.
 XX
 OS Homo sapiens.
 XX
 PN WO200204604-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-IB001770.
 XX
 PR 10-JUL-2000; 2000WO-US018777.
 PR 15-MAY-2001; 2001US-00855468.
 PR 22-JUN-2001; 2001US-00887145.
 XX
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX
 PI Kim SU;
 XX
 PS WPI; 2002-148175/19.
 XX
 DR Genetically modified human microglia cell for treating neurodegenerative
 XX disease, comprises demonstrable phagocytic properties, produces progeny
 XX in culture, presents surface antigens, and contains modified human
 XX genomic DNA.
 XX
 PS Example; Page 22; 46pp; English.
 XX
 CC The invention relates to a genetically modified human microglia cell
 CC maintained stably in vitro which has (i) has demonstrable phagocytic
 CC properties; (ii) produces progeny continuously in culture; (iii) presents
 CC CD11b and CD68 as surface antigens; and (iv) contains human genomic DNA
 CC that has been genetically modified to include a viral vector carrying at
 CC least one DNA segment encoding an exogenous gene for intracellular
 CC expression. The microglia cell line is useful for screening compounds for
 CC the treatment of autoimmune disease, and is used in the treatment of a
 CC neurodegenerative disorder e.g. Alzheimer's disease, Parkinson's disease,
 CC Huntington's disease, amyotrophic lateral sclerosis, stroke, spinal cord
 CC injuries, ataxia, brain trauma, multiple sclerosis and AIDS-(acquired
 CC immunodeficiency syndrome)-dementia. The cell line is also useful for
 CC isolating neurotoxic or neurotrophic molecules naturally produced by
 CC human microglia. The present sequence is an RT-PCR (reverse transcriptase
 CC PCR) primer which amplifies a segment of the mRNA for an expressed marker
 CC gene, used to characterise the cell line
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 434 TTACTGCTGGA 445
 |||||
 DB 9 TTACTGCTGGA 20

RESULT 278
 ABI97083/C
 ID ABI97083 standard; DNA; 20 BP.
 XX
 AC ABI97083;
 XX
 DT 16-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#4170 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010958.
 XX
 PR 14-APR-2000; 2000US-0197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zhirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 20 BP; 8 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy	584	CTTTGGGACTTT	595						
Db	20	CTTTGGGACTTT	9						

Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy	52	GTCGCTGGGCT	63						
Db	12	GTCGCTGGGCT	1						

RESULT 279

AB193909/C

ID AB193909 standard; DNA; 20 BP.

XX AC AB193909;

XX DT 16-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#996 oligo #9.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;

XX KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;

XX KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;

XX KW oncogene; tumour suppressor; human papillomavirus; forensic;

XX KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX PI WPI; 2002-034366/04.

XX DR

XX PT Designing capture oligonucleotide probes for use on a support to which

XX PT complementary oligonucleotides hybridize with little mismatch.

XX PS

XX PS Example 5; Fig 29; 300pp; English.

XX CC The present invention describes a method (M1) for designing capture

XX CC oligonucleotide probes (I) for use on a support to which complementary

XX CC oligonucleotide probes (II) will hybridize with little mismatch, where

XX CC (I) have melting temperatures within a narrow range. The method is useful

XX CC for detecting infectious diseases caused by bacterial infectious agents

XX CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal

XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and

XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,

XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents

XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus

XX CC medinensis. The method is also useful for detecting genetic diseases such

XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes

XX CC involved in DNA amplification, replication, recombination or repair, the

XX CC cancer is specifically associated with a gene selected from BRCA1 gene,

XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The

XX CC method is also used for environmental monitoring, forensics and the food

XX CC and feed industry, detecting comprises scanning (using e.g. a scanning

XX CC electron microscope and infrared microscope) the support at the

XX CC particular sites and identifying if ligation of the oligonucleotide probe

XX CC sets occurred and correlating (using a computer) identified ligation to a

XX CC presence or absence of the target nucleotide sequences. AB192074 to

XX CC AB197546 represent oligonucleotide sequences used in the exemplification

XX CC of the present invention

XX SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Example 5; Fig 29; 300pp; English.

The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridize with little mismatch, where (I) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus neoformans, Candida albicans and Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus, Epstein-Barr virus and polio virus, and parasitic infectious agents selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus medinensis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects. Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. AB182074 to AB197546 represent oligonucleotide sequences used in the exemplification of the present invention

Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 79 ACTACTCTGTC 90
Db 9 ACTACTCTGTC 20

RESULT 281
ABI95383/C
ID ABI95383 standard; DNA; 20 BP.
XX
AC ABI95383;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#2470 oligo #9.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010958.
XX
PR 14-APR-2000; 2000US-0197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI; 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. ABI82074 to
CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 154 AAGAACGGCTGC 165
Db 19 AAGAACGGCTGC 8

RESULT 282
ABK69394
ID ABK69394 standard; DNA; 20 BP.
XX
AC ABK69394;
XX
DT 15-JUL-2002 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide #146 for caspase 9 inhibition.
XX
KW Antisense compound; caspase 9; C9; hyperproliferative disorder; stroke;
KW haematopoietic disorder; cholesterol disorder; bone metabolism disorder;
KW brain injury; neurodegenerative disease; infection; inflammation; tumour;
KW phosphorothioate backbone linkage; 2'-methoxyethyl; 2'-MOE; ss.
XX
OS Mus musculus.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides, all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO200222641-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028233.
XX
PR 11-SEP-2000; 2000US-00659845.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Zhang H, Watt AT;
XX
DR WPI; 2002-351874/38.
XX
PT New antisense oligonucleotide which modulates expression of caspase 9,
XX useful to treat tumor, inflammation or to prevent infection in humans.
XX
PS Claim 26; Page 95; 145pp; English.
XX
CC The present invention relates to a new antisense compound targeted to a
CC nucleic acid molecule encoding caspase 9 (C9). The compound specifically
CC hybridises with and inhibits the expression of caspase 9. The invention
CC also describes an antisense compound that specifically hybridises with an
CC 8 nucleotide portion of an active site of the nucleic acid. The invention
CC is useful for inhibiting the expression of C9 in cells or tissues and is
CC also useful for treating an animal having a disease or condition
CC associated with C9, including a hyperproliferative, haematopoietic or
CC cholesterol disorder, bone metabolism disorder, stroke, brain injury or
CC neurodegenerative disease. The compound is commonly useful as a research
CC and diagnostics reagent. It is also useful to distinguish between
CC functions of various members of a biological pathway. The invention is
CC also be useful prophylactically e.g. to prevent or delay infection,

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CC inflammation or tumour formation. The antisense compound of the invention
 CC is often preferred over native form because of enhanced cellular uptake,
 CC enhanced affinity for nucleic acid target and increased stability in
 CC presence of nucleases. The present nucleic acid sequence represents one
 CC of a collection (ABK69249-ABK69396) of chimeric phosphorothioate
 CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings. This sequence was
 CC used in the methods of the invention for inhibition of caspase 3
 CC
 XX
 SQ Sequence 20 BP; 7 A; 2 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGGAGGAGTT 32
 |||||
 Db 5 CCGGAGGAGTT 16

RESULT 283

ABZ97922
 ID ABZ97922 standard; DNA; 20 BP.

XX AC ABZ97922;

XX DT 17-OCT-2003 (first entry)

XX DE Human RANTES oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmacological composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX FS Disclosure; SEQ ID NO 13164; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 CAAGGCTGAGCC 368
 |||||
 Db 7 CAAGGCTGAGCC 18

RESULT 284

ABZ94049/C
 ID ABZ94049 standard; DNA; 20 BP.

XX AC ABZ94049;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmacological composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX FS Disclosure; SEQ ID NO 9291; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 11 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 431 ATTTTACTGCT 442
 |||||
 Db 13 ATTTTACTGCT 2

RESULT 285
 ABZ92856/c
 ID ABZ92856 standard; DNA; 20 BP.
 XX
 AC ABZ92856;
 XX
 DT 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 DE
 DE Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX WO200285308-A2.
 PN 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013135.
 PF 24-APR-2001; 2001US-0286137P.
 PR (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 8098; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 4 A; 1 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 44 TCAAAAATGTCC 55
 |||||
 Db 15 TCAAAAATGTCC 4

RESULT 286
 ABZ89531/c
 ID ABZ89531 standard; DNA; 20 BP.
 XX
 AC ABZ89531;
 XX
 DT 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 DE
 DE Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX WO200285308-A2.
 PN 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013135.
 PF 24-APR-2001; 2001US-0286137P.
 PR (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4773; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAATGTC 54
 |||||
 Db 14 TTCAAAATGTC 3

RESULT 287

ABZ90933/c
 ID ABZ90933 standard; DNA; 20 BP.

XX AC ABZ90933;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 6175; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 7 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGGAAGTTTCT 35
 |||||
 Db 12 GAGGAAGTTTCT 1

RESULT 288

ABZ97923
 ID ABZ97923 standard; DNA; 20 BP.

XX AC ABZ97923;

XX DT 17-OCT-2003 (first entry)

XX DE Human RANTES oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Disclosure; SEQ ID NO 13165; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 357 CAAGGCTGACC 368
 |||||
 DB 2 CAAGGCTGACC 13

RESULT 289
 ABZ88197/C
 ID ABZ88197 standard; DNA; 20 BP.
 XX
 AC ABZ88197;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3439; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AGCCTCTTGATG 18
 |||||
 DB 17 AGCCTCTTGATG 6

RESULT 290
 ABZ90932/C
 ID ABZ90932 standard; DNA; 20 BP.
 XX
 AC ABZ90932;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 6174; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 5 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGGAAGTTTCT 35
 |||||
 Db 18 GAGGAAGTTTCT 7

RESULT 291
 ABZ89530/C
 ID ABZ89530 standard; DNA; 20 BP.

AC ABZ89530;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 4772; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 20 BP; 8 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGTC 54
 |||||
 Db 20 TTCAAAAATGTC 9

RESULT 292
 ABZ88369

ID ABZ88369 standard; DNA; 20 BP.

AC ABZ88369;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 3611; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 20 BP; 11 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 AAAACCATGAAA 469
 Db 5 AAAACCATGAAA 16
 |||||

RESULT 293

AC82966
 ID ACC82966 standard; DNA; 20 BP.

XX
 AC ACC82966;

XX
 DT 27-AUG-2003 (first entry)

XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198838.

XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; propylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT modified_base 1..20

FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"

FT modified_base 1..5

FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

PN W02003040328-A2.

XX
 PD 15-MAY-2003.

XX
 PF 05-NOV-2002; 2002WO-US035479.

XX
 PR 08-NOV-2001; 2001US-00008789.

XX
 PA (ISIS-) ISIS PHARM INC.

XX
 PI Bennett CF, Dobie K;

XX
 DR WPI; 2003-430662/40.

XX
 PT New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

XX
 PS Example 15; Page 78; 111pp; English.

XX
 CC The invention relates to antisense compounds targetted to a nucleic acid

CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. They are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 GGAGCCCTGCT 262

Db 4 GGAGCCCTGCT 15
 |||||

RESULT 294

AA53980

ID AA53980 standard; DNA; 20 BP.

XX
 AC AA53980;

XX
 DT 18-FEB-2003 (first entry)

XX
 DE Human serotonin 1B receptor gene PCR primer, SEQ ID No 4.

KW Single nucleotide polymorphism; analgesic; variant allele; A-161T;
 KW human serotonin 1B receptor gene; addictive disease; neurologic;
 KW psychiatric condition; pain reliever; analgesia; PCR; primer; ss.

XX
 OS Homo sapiens.

XX
 FN US2002142312-A1.

XX
 PD 03-OCT-2002.

XX
 PF 15-MAY-2001; 2001US-00855991.

XX
 PR 15-MAY-2000; 2000US-0204169P.

XX
 PA (CIGL/) CIGLER T.

XX
 PA (LAPO/) LAFORGE K S.

XX
 PA (KREE/) KREEK M J.

XX
 PI Cigler T, Laforge KS, Kreek MJ;

XX
 DR WPI; 2003-102507/09.

XX
 PT Novel isolated variant allele of human serotonin 1B receptor gene useful
 PT for determining susceptibility to addictive, neurologic or psychiatric
 PT conditions or diseases in a subject.

XX
 PS Example; Page 12; 20pp; English.

XX
 CC The invention relates to a novel isolated variant allele of the human
 CC serotonin 1B receptor gene, comprising a DNA sequence having a variation
 CC in a sequence of 1749 base pairs defined in the specification, where the
 CC variation comprises A-161T. The human serotonin 1B receptor gene is
 CC useful for determining a susceptibility in a subject to at least one
 CC addictive disease, neurologic or psychiatric condition or disease. The
 CC addictive disease comprises opioid addiction, cocaine addiction, or
 CC addiction to other psychostimulants, nicotine addiction, barbiturate or
 CC sedative hypotonic addiction, anxiolytic addiction, or alcohol addiction.
 CC The neurologic or psychiatric condition or disease is anxiety,
 CC depression, pathological aggression, or compulsive gambling. The human

```
CC serotonin 1B receptor gene is also useful for determining a therapeutic
CC amount of pain reliever to administer to the subject in order to induce
CC analgesia. This polynucleotide sequence represents a PCR primer of the
CC human serotonin 1B receptor gene of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 GACCTACCTGTG 89
Db 4 GACCTACCTGTG 15

RESULT 295
ACCTG0919
ID ACC70919 standard; DNA; 20 BP.
XX
AC ACCTG0919;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cytochrome b PCR primer #12.
XX
KW Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003033737-A1.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-JP010640.
XX
PR 17-OCT-2001; 2001JP-00318805.
XX
PA (GIFU-) GIFU INT INST BIO TECHNOLOGY.
XX
FI Tanaka M;
XX
WPI; 2003-393541/37.
XX
Gene detection method using human mitochondrial DNA to reveal and confirm
PT amino acid substitution advantageous or disadvantageous in prolonged
PT survival of human, useful for diagnosis of Parkinson's disease.
XX
PS Disclosure; Page 7; 35pp; Japanese.
XX
The present invention relates to a detection method using human
CC mitochondrial (mt) DNA. The method comprises detecting the replacement of
CC a base accompanying an amino acid substitution in a protein encoded by
CC its base sequence in a human mitochondrial DNA base sequence. The method
CC is useful for diagnosis of Parkinson's disease, and in health checks and
CC assessing risks for other adult diseases. The present sequence is a PCR
CC primer, which was used to illustrate the invention
XX
SQ Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 462 CCATGAAGAAC 473
Db 2 CCATGAAGAAC 13

RESULT 296
ABZ59472/c
ID ABZ59472 standard; DNA; 20 BP.
XX
```

```
AC ABZ59472;
XX 17-APR-2003 (first entry)
XX Human src-c chimeric phosphorothioate oligonucleotide SEQ ID NO:93.
XX
XX Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
XX antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
XX antisense oligonucleotide; aberrant bone remodeling; breast cancer;
XX hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
XX ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
XX Kaposi's sarcoma; infection; inflammation; tumour formation;
XX phosphorothioate; ss.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages"
XX modified_base 1..5
XX /tag= a
XX /mod_base= OTHER
XX modified_base 16..20
XX /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-O-methoxyethyl gapmer (2'-MOE wing)"
XX
XX WO200295053-A2.
XX
XX 28-NOV-2002.
XX
XX 16-MAY-2002; 2002WO-US015684.
XX
XX 18-MAY-2001; 2001US-00860473.
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Watt AT;
XX
XX WPI; 2003-120806/11.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding src-c,
XX useful for diagnosing, treating or preventing diseases associated with
XX the expression of src-c, e.g. cancer or inflammation, and in research
XX applications.
XX
XX Claim 3; Page 90; 137pp; English.
XX
XX The present invention describes a compound (I) that is 8-50 nucleobases
XX in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
XX coding region, intron region, exon region, stop codon, intron:exon
XX junction, exon:exon junction, or 5' mRNA variant of src-c, and which
XX specifically hybridizes with and inhibits the expression of src-c. (I)
XX have cytostatic, antiinflammatory, osteopathic and antibacterial
XX activities, and can be used in antisense therapy and in vaccines. The
XX antisense compounds (I) can be used for modulating the expression of src-
XX c and for treating diseases or conditions associated with expression of
XX src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
XX particularly cancer, such as breast cancer, pancreatic cancer, lung
XX cancer, ovarian cancer, oesophageal cancer, neuroblastoma, retinoblastoma
XX or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
XX prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
XX formation, as research reagents and kits, and in distinguishing between
XX functions of various members of a biological pathway. The present
XX sequence represents a human src-c antisense chimeric phosphorothioate
XX oligonucleotide, which is used in an example from the present invention
XX
XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
```

Query Match 2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCCGACTTT 291
DB 15 GTGGCCGACTTT 4

RESULT 297
ABT14121
ID ABT14121 standard; DNA; 20 BP.
XX AC
XX ABT14121;
XX 18-FEB-2003 (first entry)
XX Nucleic acid sequence analysis related oligonucleotide #54.
XX
XX Primary subunit sequence; variation; secondary subunit sequence;
XX sequence analysis; refractory behaviour; ds.
XX Unidentified.
XX WO200279502-A1.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-AU000397.
XX 28-MAR-2001; 2001US-0279238P.
XX (UQUU) UNIV QUEENSLAND.
XX Keith JM, Bryant DE, Adams P;
XX WPI; 2003-075457/07.
XX
XX Analyzing a primary subunit sequence, useful for sequence analysis,
XX comprises analyzing a secondary subunit sequence which varies from a
XX primary subunit sequence by an addition, deletion and/or substitution of
XX a subunit.
XX Disclosure; Page 55; 168pp; English.
XX
XX The invention relates to a novel method for analysing a primary subunit
XX sequence. The novel method comprises analysing the variation in a
XX secondary subunit sequence, which varies from the primary subunit
XX sequence by the addition, deletion and/or substitution of a subunit, to
XX infer information relative to the primary subunit sequence. The method is
XX useful in sequence analysis and for analysing subunit sequences to infer
XX or otherwise obtain information relating to a property, feature or
XX physical parameter of the subunit sequence, such as its sequence
XX information, structure, size or refractory behaviour to the execution of
XX a task. The secondary subunit sequence is used for analysing refractory
XX behaviour of the primary subunit sequence to the execution of a task, and
XX in deriving a set of subsequences for comparison with a set of
XX subsequences derived from the primary subunit sequence to facilitate the
XX deduction of the primary subunit sequence. This polynucleotide sequence
XX represents an oligonucleotide relating to the analysing method of the
XX invention
XX
XX Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 GTCCGCTGGGCT 63
DB 8 GTCCGCTGGGCT 19

RESULT 298
ACC99647
ID ACC99647 standard; DNA; 20 BP.
XX AC
XX ACC99647;
XX 02-SEP-2003 (first entry)
XX Telenc/ICA PCR primer SEQ ID NO:28.
XX Multiplex real-time quantitative PCR; PCR primer; copy number;
XX Alzheimer's disease; ss.
XX Synthetic.
XX WO2003048377-A2.
XX 12-JUN-2003.
XX 02-DEC-2002; 2002WO-US038806.
XX 30-NOV-2001; 2001US-0336095P.
XX 19-JUL-2002; 2002US-0397475P.
XX (UYRP) UNIV ROCHESTER.
XX (THER/) THERIANOS S.
XX Zhu M, Coleman P;
XX WPI; 2003-532841/50.
XX
XX Determining the relative copy number of a group of target nucleic acid
XX molecules present in a sample by performing a first or second PCR in a
XX PCR mixture and quantifying the number of copies of the second target
XX nucleic acid product.
XX
XX Example 1; Fig 8; 118pp; English.
XX
XX The present invention describes a multiplex real-time quantitative PCR
XX method for determining the relative copy number of a group of target
XX nucleic acid molecules present in a sample. The method comprises: (1)
XX performing a first PCR in a PCR mixture; (2) performing a second PCR in a
XX PCR mixture; and (3) quantifying the number of copies of the second
XX target nucleic acid product present in the sample containing the target
XX nucleic acid molecule. Also described: (1) quantifying the copy number of
XX a group of target nucleic acids in a sample; and (2) determining whether
XX a subject is at risk of acquiring Alzheimer's disease. The method is
XX useful for determining the relative copy number of a group of target
XX nucleic acid molecules present in a sample for determining whether a
XX subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
XX represent PCR primer used in the exemplification of the present invention
XX
XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 TAGACCCCTGCC 220
DB 5 TAGACCCCTGCC 16

RESULT 299
ABT43789/C
ID ABT43789 standard; DNA; 20 BP.
XX AC
XX ABT43789;
XX 16-OCT-2003 (first entry)
XX Human PTP5K1a antisense oligonucleotide Seq ID41.
XX

KW Human, phosphatidylinositol-4-phosphate 5-kinase 1alpha; PIP5K1alpha;
 KW antiinflammatory; antitumor; cytostatic; gene therapy; tumour;
 KW antisense oligonucleotide; hyperproliferative disorder;
 KW inflammatory disorder; infection; inflammation; 2'-methoxyethyl wing;
 KW 2'-MOE wing; phosphorothioate backbone; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003050309-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 04-DEC-2002; 2002WO-US038615.
 XX
 PR 06-DEC-2001; 2001US-00003354.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Freier SM;
 XX
 XX WPI; 2003-627257/59.
 DR
 XX
 XX New antisense compound useful for treating diseases such as
 PT hyperproliferative or inflammatory disorders, hybridizes and inhibits
 PT nucleic acid encoding phosphatidylinositol-4-phosphate 5-kinase, 1 alpha.
 PT
 XX
 PS Claim 3; Page 82; 117pp; English.
 XX
 XX This invention relates to the novel antisense compounds, particularly
 CC antisense oligonucleotides, for the modulation of phosphatidylinositol-4-
 CC phosphate 5-kinase 1alpha (PIP5K1a) expression. The oligonucleotides of
 CC the invention may have antiinflammatory, antitumor or cytostatic
 CC activities through use in a gene therapy method. As a result the
 CC antisense oligonucleotides may be of use for the treatment of an animal
 CC having a disease associated with PIP5K1a such as a hyperproliferative or
 CC inflammatory disorder through inhibition of PIP5K1a expression. The
 CC oligonucleotides of the invention may also be used prophylactically to
 CC prevent or delay infection, inflammation or tumour formation. They may
 CC also be useful for diagnostics, therapeutics, prevention, as research
 CC reagents and kits or for distinguishing functions of various members of a
 CC biological pathway. The present sequence is that of an antisense
 CC oligonucleotide of the invention. The oligonucleotide is a chimeric
 CC phosphorothioate oligonucleotide which has five nucleotide 2'-
 CC methoxyethyl (2'-MOE) wings with a ten nucleotide deoxynucleotide gap.
 CC The oligonucleotide backbone is phosphorothioate throughout
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 ACAGCCTCTTGA 16
 DB 12 ACAGCCTCTTGA 1
 RESULT 300
 ID ABT44205/C
 XX
 XX ABT44205 standard; DNA; 20 BP.
 AC ABT44205;
 XX
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Chimeric antisense oligonucleotide ISIS 199201 to inhibit human NOD1.
 XX
 KW Antisense; nucleotide binding oligonucleotide domain 1; gene therapy; ss;
 KW caspase associated recruitment domain 4; programmed cell death; cancer;
 KW apoptosis; Alzheimer's; neurodegenerative; Parkinson's; ALS; NOD1; CARD4;
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; autoimmune disorder;
 KW viral infection; human; chimeric.

OS Chimeric - Homo sapiens.
 XX
 PN WO2003050246-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 04-DEC-2002; 2002WO-US038606.
 XX
 PR 05-DEC-2001; 2001US-00006893.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dobie KW, Roach MP;
 XX
 XX WPI; 2003-577293/54.
 DR
 XX
 XX New compound, comprising a sequence targeted to a nucleic acid encoding
 PT nucleotide-binding oligomerization domain 1 (NOD1), useful for preparing
 PT a composition for treating hyperproliferative disease, e.g., cancer.
 PT
 XX
 XX Example 15; Page 76; 138pp; English.
 PS
 XX
 XX This invention relates to novel chimeric antisense oligonucleotides that
 CC specifically hybridize to and inhibit the expression of the nucleotide
 CC binding oligonucleotide domain 1, NOD1 protein. NOD1, also known as CARD4
 CC (caspase associated recruitment domain 4) is a domain that is involved in
 CC the elimination of cells via programmed cell death and in the host
 CC defence against pathogens, i.e. it works to regulate apoptosis. Apoptosis
 CC is a naturally occurring process, however, if it becomes overstimulated
 CC it can lead to cell loss and neurodegenerative conditions including
 CC Alzheimer's, Parkinson's, amyotrophic lateral sclerosis (ALS), retinitis
 CC pigmentosa and blood cell disorders. Conversely, insufficient apoptosis
 CC can contribute to the development of cancer, autoimmune disorders and
 CC viral infections. The present invention describes antisense
 CC oligonucleotides that can modulate NOD1 expression (and variants
 CC thereof), such that these compounds, via gene therapy, can be used to
 CC treat various human diseases caused by aberrant apoptosis. This
 CC oligonucleotide sequence is the chimeric antisense oligo used to inhibit
 CC expression of human NOD1, the aim of the invention. Note that it has two
 CC terminal five nucleotide 2'-methoxyethyl (2'-MOE) wings separated by a
 CC ten deoxynucleotide gap. The oligonucleotide backbone is phosphorothioate
 CC throughout
 XX
 SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 585 TTGGGACTTTG 596
 DB 16 TTGGGACTTTG 5
 Search completed: March 4, 2004, 22:07:19
 Job time : 376 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:53:48 ; Search time 306 seconds
(without alignments)
7135.578 Million cell updates/sec

Title: US-09-966-880A-7_COPY_80_676

Perfect score: 597

Sequence: 1 agggacagcctctgatgaa.....ttcgactttggactttga 597

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2421054 seqs, 1828716029 residues

Word size : 0

Total number of hits satisfying chosen parameters: 452776

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
C 1	15.	2.5	20	15	US-10-349-143-10030
C 2	14	2.3	20	12	Sequence 10030, A
C 3	14	2.3	20	14	Sequence 337, App
C 4	14	2.3	20	14	Sequence 4739, Ap
C 5	13	2.2	17	14	Sequence 103, App
C 6	13	2.2	17	14	Sequence 795, App
C 7	13	2.2	17	14	Sequence 796, App
C 8	13	2.2	17	14	Sequence 797, App
C 9	13	2.2	17	14	Sequence 798, App
C 10	13	2.2	17	14	Sequence 799, App
C 11	13	2.2	17	14	Sequence 2817, Ap
C 12	13	2.2	17	14	Sequence 3379, Ap
C 13	13	2.2	17	15	Sequence 1006, App
C 14	13	2.2	17	15	Sequence 103, App
C 15	13	2.2	17	15	Sequence 104, App
C 16	13	2.2	19	9	US-09-018-125-9

C 16	13	2.2	19	14	US-10-240-046A-84
C 17	13	2.2	19	15	US-10-223-507-4
C 18	13	2.2	20	9	US-09-752-983-41
C 19	13	2.2	20	10	US-09-954-679-61
C 20	13	2.2	20	14	US-10-215-112-9247
C 21	13	2.2	20	14	US-10-215-112-9359
C 22	13	2.2	20	14	US-10-215-112-9583
C 23	13	2.2	20	14	US-10-215-112-9584
C 24	13	2.2	20	14	US-10-215-112-9587
C 25	13	2.2	20	14	US-10-215-112-9752
C 26	13	2.2	20	14	US-10-215-112-9863
C 27	13	2.2	20	14	US-10-215-112-10087
C 28	13	2.2	20	14	US-10-215-112-10088
C 29	13	2.2	20	14	US-10-215-112-10091
C 30	13	2.2	20	15	US-10-005-341-41
C 31	13	2.2	20	15	US-10-154-708-45
C 32	13	2.2	20	15	US-10-154-708-109
C 33	13	2.2	20	15	US-10-177-554-75
C 34	13	2.2	20	16	US-10-210-589-59
C 35	12	2.0	15	9	US-09-767-395-35
C 36	12	2.0	15	14	US-10-203-860-22
C 37	12	2.0	16	9	US-09-881-012-129
C 38	12	2.0	16	15	US-10-629-951-41
C 39	12	2.0	17	9	US-09-866-108-7364
C 40	12	2.0	17	9	US-09-866-108-7365
C 41	12	2.0	17	9	US-09-866-108-7366
C 42	12	2.0	17	9	US-09-866-108-7367
C 43	12	2.0	17	9	US-09-866-108-7368
C 44	12	2.0	17	9	US-09-866-108-7369
C 45	12	2.0	17	9	US-09-420-433-46

ALIGNMENTS

RESULT 1

US-10-349-143-10030/c
; Sequence 10030, Application US/10349143
; Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET 020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

SEQ ID NO 10030

LENGTH: 20

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: primer_bind

LOCATION: 1..20

OTHER INFORMATION: downstream amplification primer 99-8910 for SEQ 216S, in compler

Query Match 2.5%; Score 15; DB 15; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GAGGAAGTTCTTTA 38

Db 15 GAGGAAGTTCTTTA 1

```
RESULT 2
US-10-188-186-337
; Sequence 337, Application US/10188186
; Publication No. US20040029789A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-397C
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/360814
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/303828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/323380
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/361133
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/304016
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/373881
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/305673
; PRIOR FILING DATE: 2001-07-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: Custom
; SEQ ID NO 337
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-188-186-337

Query Match      2.3%; Score 14; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      258 CTGCTACGACTGTG 271
Db      6 CTGCTACGACTGTG 19
|||||

RESULT 3
US-10-032-585-4739/c
; Sequence 4739, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4739
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4739

Query Match      2.3%; Score 14; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      352 GACCGCAAGGCTGA 365
Db      14 GACCGCAAGGCTGA 1
|||||

US-10-262-445-103
; Sequence 103, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Curasequest version 0.1
; SEQ ID NO 103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-262-445-103

Query Match      2.3%; Score 14; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 551 ATGAGGTTGATGAC 564
    |||||
Db 1 ATGAGGTTGATGAC 14

RESULT 5
US-10-060-756A-795/c
; Sequence 795, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 795
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-795

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 17 CTGCACCGCGCCG 5

RESULT 6
US-10-060-756A-796/c
; Sequence 796, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 796
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-796

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 17 CTGCACCGCGCCG 5

RESULT 7
US-10-060-756A-797/c
; Sequence 797, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 797
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-797

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 15 CTGCACCGCGCCG 3

RESULT 8
US-10-060-756A-798/c
; Sequence 798, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
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; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 796
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-796

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 16 CTGCACCGCGCCG 4

RESULT 9
US-10-060-756A-799/c
; Sequence 799, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 799
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-799

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 CTGCACCGCGCCG 397
    |||||
Db 15 CTGCACCGCGCCG 3

RESULT 10
US-10-060-756A-799/c
; Sequence 799, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 798
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-798

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCG 397
|||||
DB 14 CTGCACCGCGCG 2

RESULT 9
US-10-060-756A-799/c
; Sequence 799, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 799
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-799

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCG 397
|||||

Db 13 CTGCACCGCGCG 1
RESULT 10
US-10-238-700-2817
; Sequence 2817, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2817
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2817

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 92.3%; Pred. No. 1.8e+04;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGCTGCGCGG 384
|||||
DB 3 GGGCTGCGCGG 15

RESULT 11
US-10-238-700-3379/c
; Sequence 3379, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3379
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3379

Query Match 2.2%; Score 13; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GCAAGGCTGAGCC 368
|||||
DB 15 GCAAGGCTGAGCC 3

RESULT 12
US-10-297-068-1006
; Sequence 1006, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi

APPLICANT: KAGIYA, Taeko
APPLICANT: ICHIHARA, Tatsuo
APPLICANT: Matsumura, Yoshiyuki
APPLICANT: MORIYA, Shogo
APPLICANT: NISHIDA, Michio
TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
FILE REFERENCE: 13140P174
CURRENT APPLICATION NUMBER: US/10/297,068
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: JP 2000-164798
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 1298
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1006
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1006

Query Match 2.2%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCCACGTGG 172
|||||
DB 3 GGCTGCCACGTGG 15

RESULT 13
US-10-307-005-103/c

Sequence 103, Application US/10307005
Publication No. US20030236208A1

GENERAL INFORMATION:

APPLICANT: University of Delaware
APPLICANT: Eric B. Kmiec
APPLICANT: Howard B. Gamper
APPLICANT: Michael C. Rice
APPLICANT: Jungsup Kim

TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
Using Modified Single Stranded Oligonucleotides

FILE REFERENCE: Napro/009 PCT

CURRENT APPLICATION NUMBER: US/10/307,005

CURRENT FILING DATE: 2002-11-26

PRIOR APPLICATION NUMBER: PCT/US01/17672

PRIOR FILING DATE: 2001-06-01

PRIOR APPLICATION NUMBER: US 60/208,538

PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: US 09/818,875

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 2717

SOFTWARE: Friedman macro Napro4

SEQ ID NO 103

LENGTH: 17

TYPE: DNA

ORGANISM: Hordeum vulgare

US-10-307-005-103

Query Match 2.2%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGACCT 82
|||||
DB 16 CGCGGTGACCT 4

RESULT 14

US-10-307-005-104

Sequence 104, Application US/10307005

Publication No. US20030236208A1
GENERAL INFORMATION:
APPLICANT: University of Delaware
APPLICANT: Eric B. Kmiec
APPLICANT: Howard B. Gamper
APPLICANT: Michael C. Rice
APPLICANT: Jungsup Kim
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
Using Modified Single Stranded Oligonucleotides
FILE REFERENCE: Napro/009 PCT
CURRENT APPLICATION NUMBER: US/10/307,005
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: PCT/US01/17672
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/818,875
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 2717
SOFTWARE: Friedman macro Napro4
SEQ ID NO 104
LENGTH: 17
TYPE: DNA
ORGANISM: Hordeum vulgare
US-10-307-005-104

Query Match 2.2%; Score 13; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGACCT 82
|||||
DB 2 CGCGGTGACCT 14

RESULT 15

US-09-018-125-9

Sequence 9, Application US/09018125A

Patent No. US20010007902A1

GENERAL INFORMATION:

APPLICANT: Silverman, Robert H.

APPLICANT: Kondo, Seiji

APPLICANT: Cowell, John K.

APPLICANT: Li, Gulying

APPLICANT: Torrence, Paul F.

TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES

FILE REFERENCE: 8656-022

CURRENT APPLICATION NUMBER: US/09/018,125A

CURRENT FILING DATE: 1999-02-03

EARLIER APPLICATION NUMBER: 60/044,507

EARLIER FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide

US-09-018-125-9

Query Match 2.2%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407
|||||
DB 3 CCGGGGTGCAAT 15

RESULT 16
US-10-240-046A-84/c
; Sequence 84, Application US/10240046A
; Publication No. US20030190639A1
; GENERAL INFORMATION:
; APPLICANT: HUGOT, JEAN-PIERRE
; APPLICANT: THOMAS, GILLES
; APPLICANT: ZOULALI, MOHAMED
; APPLICANT: LESAGE, SUZANNE
; APPLICANT: CHAMAILLARD, MATHIAS
; TITLE OF INVENTION: GENES INVOLVED IN INTESTINAL INFLAMMATORY DISEASES AND USE THEREOF
; FILE REFERENCE: 37991-0009
; CURRENT APPLICATION NUMBER: US/10/240,046A
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: PCT/FR 01/00935
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: FR 00/03832
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-240-046A-84

Query Match 2.2%; Score 13; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TCCGCTGGGCTAA 65
DB 18 TCCGCTGGGCTAA 6

RESULT 17
US-10-223-507-4/c
; Sequence 4, Application US/10223507
; Publication No. US20030207287A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
; CURRENT APPLICATION NUMBER: US/10/223,507
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/495,052
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-10-223-507-4

Query Match 2.2%; Score 13; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+04; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCTCTCCA 520
DB 15 GTTCGTCTCTCCA 3

RESULT 18
US-09-752-983-41/c
; Sequence 41, Application US/09752983
; Patent No. US20010016575A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,983
; FILING DATE: 02-Jan-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/280,805
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-752-983-41

Query Match 2.2%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376
DB 19 GAGCCCGAGGGGC 7

RESULT 19
US-09-954-679-61
; Sequence 61, Application US/09954679
; Publication No. US20030100522A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIBONUCLEASE L (2',5'-OLIGOISODENYLATE
; TITLE OF INVENTION: SYNTHETASE-DEPENDENT) EXPRESSION
; FILE REFERENCE: RYS-0212
; CURRENT APPLICATION NUMBER: US/09/954,679
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 88

```

; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-954-679-61

Query Match      2.2%; Score 13; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 AGTCTGAGGATCT 325
Db 1 AGTCTGAGGATCT 13

RESULT 20
US-10-215-112-9247/c
; Sequence 9247, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9247
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9247

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
Db 15 AGACCTACCTGTG 3

RESULT 21
US-10-215-112-9359/c
; Sequence 9359, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9359
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9359

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
Db 15 AGACCTACCTGTG 3

RESULT 22
US-10-215-112-9583/c
; Sequence 9583, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9583
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9583

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
Db 15 AGACCTACCTGTG 3

RESULT 23
US-10-215-112-9584/c
; Sequence 9584, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9584
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9584

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACCTACCTGTG 89
Db 15 AGACCTACCTGTG 3

RESULT 24
US-10-215-112-9587/c
; Sequence 9587, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9587

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```

; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9587
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9587

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      6 AGACCTACCTGTG 18

RESULT 25
US-10-215-112-9752
; Sequence 9752, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9752
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9752

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      15 AGACCTACCTGTG 3

RESULT 26
US-10-215-112-9863
; Sequence 9863, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9863
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-9863

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      6 AGACCTACCTGTG 18

RESULT 27
US-10-215-112-10087
; Sequence 10087, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10087
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10087

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      6 AGACCTACCTGTG 18

RESULT 28
US-10-215-112-10088
; Sequence 10088, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10088
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10088

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      6 AGACCTACCTGTG 18

RESULT 29
US-10-215-112-10091
; Sequence 10091, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: Test3
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10091

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      77 AGACCTACCTGTG 89
      |||||
DB      6 AGACCTACCTGTG 18

```

```
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10091
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-10091

Query Match      2.2%; Score 13; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 AGACTTACTGTG 89
Db 6 AGACTTACTGTG 18

RESULT 30
US-10-005-344-41/c
; Sequence 41, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Rich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-41

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7

RESULT 31
US-10-154-708-45
; Sequence 45, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109/c
; Sequence 109, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTTTACTGCT 442
Db 5 TATTTTACTGCT 17

RESULT 32
US-10-154-708-109/c
; Sequence 109, Application US/10154708
; Publication No. US20030219895A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CDC-LIKE KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0213
; CURRENT APPLICATION NUMBER: US/10/154,708
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-154-708-109

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 TATTTTACTGCT 442
Db 16 TATTTTACTGCT 4

RESULT 33
US-10-177-554-75
; Sequence 75, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-75

Query Match      2.2%; Score 13; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 TGGAGCCCTGCT 262
Db 1 TGGAGCCCTGCT 13
```

RESULT 34
US-10-210-589-59/c
; Sequence 59, Application US/10210589
; Publication No. US20040023381A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP2R1A EXPRESSION
; FILE REFERENCE: PTS-0041
; CURRENT APPLICATION NUMBER: US/10/210,589
; CURRENT FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 122
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-589-59

Query Match 2.2%; Score 13; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+04; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0

Qy 237 CTGGTTCACCTCC 249
Db 14 CTGGTTCACCTCC 2

RESULT 35
US-09-767-395-35
; Sequence 35, Application US/09767395
; Patent No. US2002000421S1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; Derbyshire, Elaine J
; McCafferty, John G
; Vaughan, Tristan J
; Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/767,395
; FILING DATE: 23-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/098,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34800
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-767-395-35

Query Match 2.0%; Score 12; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0

Qy 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 36
US-10-203-860-22
; Sequence 22, Application US/10203860
; Publication No. US20030108904A1
; GENERAL INFORMATION:
; APPLICANT: WAKAMIYA, No. US20030108904A1utaka
; TITLE OF INVENTION: No. US20030108904A1el Scavenger Receptor
; FILE REFERENCE: 19036/38693
; CURRENT APPLICATION NUMBER: US/10/203,860
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 2000-35155
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 2000-309068
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 22
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a lambda gt11 5' Sequencing Primer.
US-10-203-860-22

Query Match 2.0%; Score 12; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0

Qy 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 37
US-09-881-012-129/c
; Sequence 129, Application US/09881012
; Publication No. US20020192655A1
; GENERAL INFORMATION:
; APPLICANT: Gims, Edward I.
; APPLICANT: Egeand, Janice A.
; APPLICANT: Paul, Steven M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Susceptibility and Resistance Genes for
; TITLE OF INVENTION: Bipolar Affective Disorder
; FILE REFERENCE: 015280-248110US
; CURRENT APPLICATION NUMBER: US/09/881,012
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US/09/175,158
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/062,924
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 240

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 129
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D4S1564 forward primer
US-09-881-012-129

Query Match 2.0%; Score 12; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 TTCACTCTCTGG 252
|||
Db 15 TTCACTCTCTGG 4

RESULT 38

US-10-629-951-41/C
; Sequence 41, Application US/10629951
; Publication No. US20040018550A1
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detection of Transition
; FILE REFERENCE: FCCC 96-21
; CURRENT APPLICATION NUMBER: US/10/629,951
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US/09/629,222A
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-629-951-41

Query Match 2.0%; Score 12; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 CTACATCCTTTT 127
|||
Db 15 CTACATCCTTTT 4

RESULT 39

US-09-866-108-7364
; Sequence 7364, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7364
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7364

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
|||
Db 6 GAAATTCAGTT 17

RESULT 40

US-09-866-108-7365
; Sequence 7365, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7365
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7365

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e-04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510
|||||
Db 5 GAAATTCAGTT 16

RESULT 41

US-09-866-108-7366
; Sequence 7366, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7367

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7366
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7366

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e-04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510
|||||
Db 4 GAAATTCAGTT 15

RESULT 42

US-09-866-108-7367
; Sequence 7367, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7367

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7367

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
|||||
Db 3 GAAATTCAGTT 14

RESULT 43

US-09-866-108-7368
; Sequence 7368, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7368
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7368

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510

Db 2 GAAATTCAGTT 13
|||||

RESULT 44

US-09-866-108-7369
; Sequence 7369, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7369
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7369

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
|||||
Db 1 GAAATTCAGTT 12

RESULT 45

US-09-420-433-46
; Sequence 46, Application US/09420433
; Patent No. US20020098480A1
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David

;; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
;; TITLE OF INVENTION: HISTOLOGIC TISSUE
;; NUMBER OF SEQUENCES: 82
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Spensley Horn Jubas & Lubitz
;; STREET: 1880 Century Park East, Suite 500
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/420,433
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/181,664
;; FILING DATE: JANUARY 14, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wetherell, Jr., Ph.D., John R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: PD-3055
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 46:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..17
US-09-420-433-46

Query Match 2.0%; Score 12; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGCGTCGATCAA 501
|||
Db 5 GGCGTCGATCAA 16

RESULT 46
US-09-730-289B-166
; Sequence 166, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 166
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-166

Query Match 2.0%; Score 12; DB 10; Length 17;

Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
Qy 428 ATTATTTTACT 439
|:|:|:|:|:|:
Db 6 AUUAUUUUUACU 17

RESULT 47
US-09-730-289B-167
; Sequence 167, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 167
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-167

Query Match 2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 428 ATTATTTTACT 439
|:|:|:|:|:|:
Db 4 AUUAUUUUUACU 15

RESULT 48
US-09-730-289B-168
; Sequence 168, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 168
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-168

Query Match 2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 33.3%; Pred. No. 6.5e+04;
Matches 4; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 428 ATTATTTTACT 439
|:|:|:|:|:|:
Db 3 AUUAUUUUUACU 14

RESULT 49
US-09-730-289B-169
; Sequence 169, Application US/09730289B

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 50							
US-09-730-289B-170							
Sequence 170, Application US/09730289B							
Publication No. US20030050259A1							
GENERAL INFORMATION:							
APPLICANT: Ribozyme Pharmaceuticals, Inc.							
APPLICANT: Blatt, Larry							
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease							
FILE REFERENCE: MEH000-864-A (400/006)							
CURRENT APPLICATION NUMBER: US/09730,289B							
CURRENT FILING DATE: 2000-12-05							
PRIOR FILING DATE: 1999-12-06							
NUMBER OF SEQ ID NOS: 3897							
SOFTWARE: Patent in version 3.0							
SEQ ID NO 169							
LENGTH: 17							
TYPE: RNA							
ORGANISM: Homo sapiens							
US-09-730-289B-169							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	33.3%	2.0%	12	10	8	0	0
Matches	4	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 51							
US-09-818-875-163							
Sequence 163, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kntec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818, 875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	1	AUUAUUUUUACU	12				
RESULT 52							
US-09-818-875-164/c							
Sequence 164, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kntec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818, 875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	1	AUUAUUUUUACU	12				

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 50							
US-09-730-289B-170							
Sequence 170, Application US/09730289B							
Publication No. US20030050259A1							
GENERAL INFORMATION:							
APPLICANT: Ribozyme Pharmaceuticals, Inc.							
APPLICANT: Blatt, Larry							
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease							
FILE REFERENCE: MEH000-864-A (400/006)							
CURRENT APPLICATION NUMBER: US/09730,289B							
CURRENT FILING DATE: 2000-12-05							
PRIOR FILING DATE: 1999-12-06							
NUMBER OF SEQ ID NOS: 3897							
SOFTWARE: Patent in version 3.0							
SEQ ID NO 169							
LENGTH: 17							
TYPE: RNA							
ORGANISM: Homo sapiens							
US-09-730-289B-169							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	33.3%	2.0%	12	10	8	0	0
Matches	4	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 51							
US-09-818-875-163							
Sequence 163, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kmiec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
TITLE OF INVENTION: Stranded Oligonucleotides							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818,875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	10	0	0	0
Matches	12	Conservative	0	Indels	0	0	0
Qy	428	ATTATTTTACT	439				
Db	1	AUUAUUUUUACU	12				
RESULT 52							
US-09-818-875-164/c							
Sequence 164, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kmiec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
TITLE OF INVENTION: Stranded Oligonucleotides							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818,875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	10	0	0	0
Matches	12	Conservative	0	Indels	0	0	

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	Indels	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 50							
US-09-730-289B-170							
Sequence 170, Application US/09730289B							
Publication No. US20030050259A1							
GENERAL INFORMATION:							
APPLICANT: Ribozyme Pharmaceuticals, Inc.							
APPLICANT: Blatt, Larry							
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease							
FILE REFERENCE: MEH000-864-A (400/006)							
CURRENT APPLICATION NUMBER: US/09730,289B							
CURRENT FILING DATE: 2000-12-05							
PRIOR FILING DATE: 1999-12-06							
NUMBER OF SEQ ID NOS: 3897							
SOFTWARE: Patent in version 3.0							
SEQ ID NO 169							
LENGTH: 17							
TYPE: RNA							
ORGANISM: Homo sapiens							
US-09-730-289B-169							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	33.3%	2.0%	12	10	8	0	0
Matches	4	Conservative	0	Indels	0	Indels	0
Qy	428	ATTATTTTACT	439				
Db	2	AUUAUUUUUACU	13				
RESULT 51							
US-09-818-875-163							
Sequence 163, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kntec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818, 875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	Indels	0
Qy	428	ATTATTTTACT	439				
Db	1	AUUAUUUUUACU	12				
RESULT 52							
US-09-818-875-164/c							
Sequence 164, Application US/09818875							
Publication No. US20030051270A1							
GENERAL INFORMATION:							
APPLICANT: Kntec, Eric B.							
APPLICANT: Gamper, Howard B.							
APPLICANT: Rice, Michael C.							
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single							
FILE REFERENCE: Napro-4							
CURRENT APPLICATION NUMBER: US/09/818, 875							
CURRENT FILING DATE: 2001-03-27							
PRIOR APPLICATION NUMBER: US 60/192,176							
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
2.0%	100.0%	2.0%	12	17	0	0	0
Matches	12	Conservative	0	Indels	0	Indels	0
Qy	428	ATTATTTTACT	439				
Db	1	AUUAUUUUUACU	12				

; CURRENT APPLICATION NUMBER: US/09/818,875
 ; CURRENT FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 191
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-818-875-191

Query Match 2.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 Db 2 ATGAACCGGAGG 13

RESULT 54
 US-09-818-875-192/c
 ; Sequence 192, Application US/09818875
 ; Publication No. US20030051270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; APPLICANT: Rice, Michael C.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/09/818,875
 ; CURRENT FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 192
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-818-875-192

Query Match 2.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 Db 16 ATGAACCGGAGG 5

RESULT 55
 US-09-818-875-191/c
 ; Sequence 51, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim

; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MEHB00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-51

Query Match 2.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
 |||||
 Db 17 CTGAGCCCGAGG 6

RESULT 56
 US-09-780-533A-947/c
 ; Sequence 947, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MEHB00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 947
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-947

Query Match 2.0%; Score 12; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
 |||||
 Db 12 CTGAGCCCGAGG 1

RESULT 57
 US-09-780-533A-1846/c
 ; Sequence 1846, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MEHB00,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797

```
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1846

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      362 CTGAGCCCGGAGG 373
DB      14 CTGAGCCCGGAGG 3

RESULT 58
US-09-780-533A-2420/c
; Sequence 2420, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH900.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2420
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2420

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      362 CTGAGCCCGGAGG 373
DB      16 CTGAGCCCGGAGG 5

RESULT 59
US-09-780-533A-2421/c
; Sequence 2421, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEH900.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2421
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-09-780-533A-2421

Query Match      2.0%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      362 CTGAGCCCGGAGG 373
DB      15 CTGAGCCCGGAGG 4

RESULT 60
US-10-060-756A-794/c
; Sequence 794, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 794
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-794

Query Match      2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      386 TGCACCGCGCGCG 397
DB      17 TGCACCGCGCGCG 6

RESULT 61
US-10-060-756A-800/c
; Sequence 800, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
```

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/327,898
;; PRIOR FILING DATE: 2001-10-09
;; NUMBER OF SEQ ID NOS: 4804
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 800
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-756A-800

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 385 CTGCACCGCGCC 396
Db 12 CTGCACCGCGCC 1

RESULT 62

US-10-060-895A-804
;; Sequence 804, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/315,984
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 805
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-805

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 CCACGTGGAATT 176
Db 6 CCACGTGGAATT 17

US-10-060-895A-804
;; Sequence 804, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 804
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-805

RESULT 63

US-10-060-895A-805
;; Sequence 805, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/315,984
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 805
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-805

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 CCACGTGGAATT 176
Db 5 CCACGTGGAATT 16

RESULT 64

US-10-060-895A-806
;; Sequence 806, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 806
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-806

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 165 CCACGTGGAATT 176
Db 6 CCACGTGGAATT 17

;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/315,984
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 806
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-806

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176
|||||
DB 4 CCACGTGGAATT 15

RESULT 65
US-10-060-895A-807
;; Sequence 807, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 10
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/315,984
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 807
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-807

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176
|||||
DB 3 CCACGTGGAATT 14

RESULT 66
US-10-060-895A-808
;; Sequence 808, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/315,984
;; PRIOR FILING DATE: 2001-08-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 808
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-808

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176
|||||
DB 2 CCACGTGGAATT 13

RESULT 67
US-10-060-895A-809
;; Sequence 809, Application US/10060895A
;; Publication No. US20030104403A1
;; GENERAL INFORMATION:
;; APPLICANT: Zhang, Jian
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Cung-Tuong
;; TITLE OF INVENTION: HUMAN UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE 1
;; FILE REFERENCE: PB0158
;; CURRENT APPLICATION NUMBER: US/10/060,895A
;; CURRENT FILING DATE: 2002-06-10
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; NUMBER OF SEQ ID NOS: 1682
;; SOFTWARE: Aecomica Sequence Listing Engine
;; SEQ ID NO 809
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-895A-809

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/315,984
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 1682
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 809
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-895A-809

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGGAATT 176
|||||
Db 1 CCACGTGGAATT 12

RESULT 68
US-10-238-700-2816
; Sequence 2816, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2816
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2816

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 91.7%; Pred. No. 6.5e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTCGGCG 383
|||||
Db 6 GGGGCTCGGCG 17

RESULT 69
US-10-238-700-2818
; Sequence 2818, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10

; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2818
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2818

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 91.7%; Pred. No. 6.5e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGGCTCGGCGG 384
|||||
Db 1 GGGCTCGGCGG 12

RESULT 70
US-10-238-700-3223/c
; Sequence 3223, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3223
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3223

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CTGTGCCCGACA 278
|||||
Db 14 CTGTGCCCGACA 3

RESULT 71
US-10-238-700-3224/c
; Sequence 3224, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MEHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3224
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3224

Query Match 2.0%; Score 12; DB 14; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 267 CTGTGCGCGACA 278
Db 12 CTGTGCGCGACA 1

RESULT 72
US-10-238-700-3427/c
; Sequence 3427, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3427
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3427

Query Match 2.0%; Score 12; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 303 CCCCAACCTCAG 314
Db 15 CCCCAACCTCAG 4

RESULT 73
US-10-209-787-163
; Sequence 163, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/918,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 163
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-163

Query Match 2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 ATGAACCGGAGG 27
Db 15 ATGAACCGGAGG 4

RESULT 74
US-10-209-787-164/c
; Sequence 164, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 164
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-164

Query Match 2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 ATGAACCGGAGG 27
Db 15 ATGAACCGGAGG 4

RESULT 75
US-10-209-787-191
; Sequence 191, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 191

Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 ATGAACCGGAGG 27
Db 3 ATGAACCGGAGG 14

RESULT 76
US-10-209-787-164/c
; Sequence 164, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 164
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-164

Query Match 2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 ATGAACCGGAGG 27
Db 15 ATGAACCGGAGG 4

RESULT 77
US-10-209-787-191
; Sequence 191, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 191

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-191

Query Match      2.0%  Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
Db 2 ATGAACCGGAGG 13

RESULT 76
US-10-209-787-192/c
; Sequence 192, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 192
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-192

Query Match      2.0%  Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
Db 16 ATGAACCGGAGG 5

RESULT 77
US-10-261-185-163
; Sequence 163, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27

; PRIORITY APPLICATION NUMBER: US/10/261,185
; Sequence 164, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 164
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-164

Query Match      2.0%  Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
Db 15 ATGAACCGGAGG 4

RESULT 79
US-10-261-185-191
; Sequence 191, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
```

```
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 191
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-191

Query Match          2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      2 ATGAACCGGAGG 13

RESULT 80
US-10-261-185-192/c
; Sequence 192, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CCN
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 192
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-192

Query Match          2.0%; Score 12; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      16 ATGAACCGGAGG 5

RESULT 81
US-09-942-588A-42/c
; Sequence 42, Application US/09942588A
; Patent No. US20020106667A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Screening method for gene variation
; FILE REFERENCE: CFO 15717
; CURRENT APPLICATION NUMBER: US/09/942,588A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263396
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-588A-42

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 82
US-09-942-588A-65
; Sequence 65, Application US/09942588A
; Patent No. US20020106667A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Screening method for gene variation
; FILE REFERENCE: CFO 15717
; CURRENT APPLICATION NUMBER: US/09/942,588A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263396
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 67
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: p53 fragment
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-588A-65

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      1 ATGAACCGGAGG 12

RESULT 83
US-09-764-420A-1
; Sequence 1, Application US/09764420A
; Patent No. US20020115072A1
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadaashi
; APPLICANT: Yamamoto, No. US20020115072A1uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
```

```
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-1

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 84
US-09-764-420A-43/c
; Sequence 43, Application US/09764420A
; Patent No. US20020115072A1
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20020115072A1uko
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-43

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
      |||||
Db      18 ATGAACCGGAGG 7

RESULT 85
US-09-875-573-8
; Sequence 8, Application US/09875573
; Patent No. US20020150902A1
; GENERAL INFORMATION:
; APPLICANT: Tarr, Phillip I.
; TITLE OF INVENTION: POLYMORPHIC LOCI THAT DIFFERENTIATE
; TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 FROM OTHER STRAINS
; FILE REFERENCE: CHMED.001C1
; CURRENT APPLICATION NUMBER: US/09/875,573
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US99/29149
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/111,493
; PRIOR FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: primer
US-09-875-573-8

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      186 CCGCTACATCTC 197
      |||||
Db      4 CCGCTACATCTC 15

RESULT 86
US-09-942-596A-42/c
; Sequence 42, Application US/09942596A
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Method of analyzing base sequence of nucleic acid
; FILE REFERENCE: CPO 15718
; CURRENT APPLICATION NUMBER: US/09/942,596A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 263506/2000
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-596A-42

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      16 ATGAACCGGAGG 27
      |||||
Db      18 ATGAACCGGAGG 7

RESULT 87
US-09-942-596A-65
; Sequence 65, Application US/09942596A
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Canon INC.
; TITLE OF INVENTION: Method of analyzing base sequence of nucleic acid
; FILE REFERENCE: CPO 15718
; CURRENT APPLICATION NUMBER: US/09/942,596A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 263506/2000
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: p53 fragment
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-596A-65

Query Match      2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      16 ATGAACCGGAGG 27
Db      1 ATGAACCGGAGG 12

RESULT 88
US-09-988-873A-42/c
; Sequence 42, Application US/09988873A
; Publication No. US20030027160A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/09/988,873A
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
US-09-988-873A-42

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 89
US-09-988-873A-65
; Sequence 65, Application US/09988873A
; Publication No. US20030027160A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/09/988,873A
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
US-09-988-873A-65

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      1 ATGAACCGGAGG 12

RESULT 90
US-09-972-115A-17
; Sequence 17, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
```

```
; APPLICANT: Walter, Funk D.
; APPLICANT: Misczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-972-115A-17

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGGCC 257
Db      3 CTCCTGGAGGCC 14

RESULT 91
US-09-942-662A-42/c
; Sequence 42, Application US/09942662A
; Publication No. US20030190612A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: An assay of many samples for multiple items at the same time
; FILE REFERENCE: 3912041
; CURRENT APPLICATION NUMBER: US/09/942,662A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263395
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263505
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-09-942-662A-42

Query Match      2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
Db      18 ATGAACCGGAGG 7

RESULT 92
US-09-764-420A-1
; Sequence 1, Application US/09764420A
; Publication No. US20030198952A9
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20030198952A9uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
```

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; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-1

Query Match          2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 93
US-09-764-420A-43/c
; Sequence 43, Application US/09764420A
; Publication No. US20030198952A9
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Yamamoto, No. US20030198952A9uko
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Probe Bound Substrate, Process For
; TITLE OF INVENTION: Manufacturing Same, Probe Array, Method Of
; TITLE OF INVENTION: Detecting Target Substance, Method Of
; TITLE OF INVENTION: Specifying Nucleotide Sequence Of Single-
; TITLE OF INVENTION: Stranded Nucleic Acid In Sample, And
; TITLE OF INVENTION: Quantitative Determination Of Target Substance
; TITLE OF INVENTION: In Sample
; FILE REFERENCE: 35C.15258
; CURRENT APPLICATION NUMBER: US/09/764,420A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Probe Sequence
US-09-764-420A-43

Query Match          2.0%; Score 12; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 94
US-10-231-302-42/c
; Sequence 42, Application US/10231302
; Publication No. US20030082602A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20030082602A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for analyzing base sequence of nucleic acid
```

```
; FILE REFERENCE: 03500.015203
; CURRENT APPLICATION NUMBER: US/10/231,302
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP00/07244
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-302-42

Query Match          2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      18 ATGAACCGGAGG 7

RESULT 95
US-10-231-302-65
; Sequence 65, Application US/10231302
; Publication No. US20030082602A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20030082602A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for analyzing base sequence of nucleic acid
; FILE REFERENCE: 03500.015203
; CURRENT APPLICATION NUMBER: US/10/231,302
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP00/07244
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-302-65

Query Match          2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGAACCGGAGG 27
      |||||
Db      1 ATGAACCGGAGG 12

RESULT 96
US-10-128-463-10
; Sequence 10, Application US/10128463
; Publication No. US20030171314A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Department of Agriculture, Agricultural Research Service
; APPLICANT: Grubman, Marvin J.
; APPLICANT: Chingsamaram, Jarasvech
; APPLICANT: Koster, Marla
; APPLICANT: Moraes, Mauro P.
; TITLE OF INVENTION: Foot and Mouth Disease Virus Vaccine
; FILE REFERENCE: D.N. 0128.01
; CURRENT APPLICATION NUMBER: US/10/128,463
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/286,345
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
```



```
; TYPE: DNA
; ORGANISM: Porcine
US-10-128-463-10

Query Match      2.0%; Score 12; DB 14; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 CCCCAACCTCAG 314
Db 5 CCCCAACCTCAG 16

RESULT 97
US-10-418-552-128
; Sequence 128, Application US/10418552
; Publication No. US20030233672A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; APPLICANT: VAN BENENNAAM, Alison
; APPLICANT: VENKATRAHESH, Mylavaram
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR REGULATION OF PLANT GAMMA-
; TITLE OF INVENTION: TOCOPHEROL METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029 (S29-US1)
; CURRENT APPLICATION NUMBER: US/10/418,552
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,488
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/385,992
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/442,470
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 128
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cGMT reverse primer
US-10-418-552-128

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGCC 256
Db 6 CCTCCTGGAGCC 17

RESULT 98
US-10-608-804-42/c
; Sequence 42, Application US/10608804
; Publication No. US20040014124A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, No. US20040014124A1uko
; APPLICANT: Okamoto, Tadashi
; APPLICANT: Shimizu, Satoshi
; APPLICANT: Suzuki, Tomohiro
; TITLE OF INVENTION: Method for Examining Reactivity and Method for Detecting a Comple
; FILE REFERENCE: 03500.015716.1
; CURRENT APPLICATION NUMBER: US/10/608,804
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US/09/942,662
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263395
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: JP 2000-263505
; PRIOR FILING DATE: 2000-08-31
```

```
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sample oligonucleotide
US-10-608-804-42

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27
Db 18 ATGAACCGGAGG 7

RESULT 99
US-10-634-510-42/c
; Sequence 42, Application US/10634510
; Publication No. US20040018552A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/10/634,510
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-10-634-510-42

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGGAGG 27
Db 18 ATGAACCGGAGG 7

RESULT 100
US-10-634-510-65
; Sequence 65, Application US/10634510
; Publication No. US20040018552A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Terminal labelled probe array and method of making it
; FILE REFERENCE: CF015961
; CURRENT APPLICATION NUMBER: US/10/634,510
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: JP2000-357446
; PRIOR FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 65
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-10-634-510-65

Query Match      2.0%; Score 12; DB 15; Length 18;
Best Local Similarity 100.0%; Pred.No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 16 ATGACCGGAGG 27
| | | | | | | | | |
Db 1 ATGACCGGAGG 12

RESULT 101

US-10-444-206-293/c
; Sequence 293, Application US/10444206
; Publication No. US2004003917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karas, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 293
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-293

Query Match 2.0%; Score 12; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGGCTGAGGCC 369
| | | | | | | | | |
Db 14 AAGGCTGAGGCC 3

RESULT 102

US-09-805-177-7
; Sequence 7, Application US/09805177
; Patent No. US20020001805A1
; GENERAL INFORMATION:
; APPLICANT: Richard Bruce Roden
; APPLICANT: Honami Naora
; TITLE OF INVENTION: IMMUNOGENIC OVARIAN CANCER GENES
; FILE REFERENCE: 031787.0090
; CURRENT APPLICATION NUMBER: US/09/805,177
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,226
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/259,452
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers
US-09-805-177-7

Query Match 2.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
| | | | | | | | | |
Db 8 TGAGGATCTTCA 19

RESULT 103

US-09-068-817-7/c
; Sequence 7, Application US/09068817
; Patent No. US20020081733A1
; GENERAL INFORMATION:
; APPLICANT: Verfaillie, C.M.
; APPLICANT: McIvor, R.S.
; APPLICANT: Zhou, R.C.
; TITLE OF INVENTION: Method to prepare drug-resistant, non-malignant hematopoietic ce
; FILE REFERENCE: 600.347US2
; CURRENT APPLICATION NUMBER: US/09/068,817
; CURRENT FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/US96/18273
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: US 60/006,692
; PRIOR FILING DATE: 1995-11-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-068-817-7

Query Match 2.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
| | | | | | | | | |
Db 19 TGAGGATCTTCA 8

RESULT 104

US-09-068-817-8/c
; Sequence 8, Application US/09068817
; Patent No. US20020081733A1
; GENERAL INFORMATION:
; APPLICANT: Verfaillie, C.M.
; APPLICANT: McIvor, R.S.
; APPLICANT: Zhou, R.C.
; TITLE OF INVENTION: Method to prepare drug-resistant, non-malignant hematopoietic ce
; FILE REFERENCE: 600.347US2
; CURRENT APPLICATION NUMBER: US/09/068,817
; CURRENT FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/US96/18273
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: US 60/006,692
; PRIOR FILING DATE: 1995-11-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-068-817-8

Query Match 2.0%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
| | | | | | | | | |
Db 19 TGAGGATCTTCA 8

RESULT 105

```
US-10-224-005-29/c
; Sequence 29, Application US/10224005
; Publication No. US20030343732A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Posnaugh, Kathy
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD)
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/041 (MBHB01-1110-A)
; CURRENT APPLICATION NUMBER: US/10/224,005
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 347
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense 1
US-10-224-005-29
Query Match 2.0%; Score 12; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 CCGGTTACCT 247
Db 19 CCGGTTACCT 8

RESULT 106
US-10-224-005-190
; Sequence 190, Application US/10224005
; Publication No. US20030343732A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Posnaugh, Kathy
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD)
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/041 (MBHB01-1110-A)
; CURRENT APPLICATION NUMBER: US/10/224,005
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 347
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-224-005-190
Query Match 2.0%; Score 12; DB 14; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.5e+04;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 236 CCGGTTACCT 247
Db 1 CCGGUUACCU 12

RESULT 107
US-10-423-311-19/c
; Sequence 19, Application US/10423311
; Publication No. US20030206938A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Heloise Anne
; APPLICANT: Chodosh, James
; APPLICANT: Callegan, Michelle C.
; TITLE OF INVENTION: TREATMENT AND INHIBITION OF OCULAR INFECTIONS AND WOUNDS BY CAP:
; TITLE OF INVENTION: CAP37 PEPTIDES
; FILE REFERENCE: 6267.002
; CURRENT APPLICATION NUMBER: US/10/423,311
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/378,295
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Completely synthesized
US-10-423-311-19
Query Match 2.0%; Score 12; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 317 TGAGGATCTTCA 328
Db 19 TGAGGATCTTCA 8

RESULT 108
US-10-349-143-11302/c
; Sequence 11302, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11302
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19_bind
; OTHER INFORMATION: downstream amplification primer 99-4077 for SEQ 3437, in complem
US-10-349-143-11302
Query Match 2.0%; Score 12; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTCC 187
Db 15 TGCTCTTCCTCC 4

RESULT 109
US-10-352-179-5/c
; Sequence 5, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
```

APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Oryza minuta
US-10-352-179-5

Query Match 2.0%; Score 12; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TCCTCCGCTACA 193
Db 17 TCCTCCGCTACA 6

RESULT 110
US-09-802-669-21/c
Sequence 21, Application US/09802669
Patent No. US2002004490A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-802-669-21

Query Match 2.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGCTCTT 182
Db 20 GGAATTGCTCTT 9

RESULT 111
US-09-887-145-18
Sequence 18, Application US/09887145
Publication No. US20030082139A1
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia cell and continuous cell line
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387

APPLICANT: Wang, Guo-liang
APPLICANT: Liu, Guifu
TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla
FILE REFERENCE: 22727/04108
CURRENT APPLICATION NUMBER: US/10/352,179
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/352,106
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Oryza minuta
US-10-352-179-5

Query Match 2.0%; Score 12; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TCCTCCGCTACA 193
Db 17 TCCTCCGCTACA 6

RESULT 110
US-09-802-669-21/c
Sequence 21, Application US/09802669
Patent No. US2002004490A1
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-802-669-21

Query Match 2.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGCTCTT 182
Db 20 GGAATTGCTCTT 9

RESULT 111
US-09-887-145-18
Sequence 18, Application US/09887145
Publication No. US20030082139A1
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia cell and continuous cell line
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387

CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft Word version 97
CURRENT APPLICATION NUMBER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-887-145-18

Query Match 2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGGA 445
Db 9 TTACTGCTGGA 20

RESULT 112
US-09-910-185-34
Sequence 34, Application US/09910185
Publication No. US20030083279A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3 EXPRESSION
FILE REFERENCE: RFS-0258
CURRENT APPLICATION NUMBER: US/09/910,185
CURRENT FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 34
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-910-185-34

Query Match 2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGAC 354
Db 9 TTCTGTGAGGAC 20

RESULT 113
US-09-851-871-14
Sequence 14, Application US/09851871
Publication No. US20030176374A1
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank

```
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0543
; CURRENT APPLICATION NUMBER: US/09/851,871
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-14

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
Db 6 TCCTGGAGCCCC 17

RESULT 114
US-09-851-871-198
; Sequence 198, Application US/09851871
; Publication No. US20030176374A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0543
; CURRENT APPLICATION NUMBER: US/09/851,871
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-198

Query Match      2.0%; Score 12; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
Db 5 TCCTGGAGCCCC 16

RESULT 115
US-10-619-220-21/c
; Sequence 21, Application US/10619220
```

```
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-619-220-21

Query Match      2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTCGCTCTT 182
Db 20 GGAATTCGCTCTT 9

RESULT 116
US-10-068-160-43/c
; Sequence 43, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-43

Query Match      2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 CCCCTGCTACGA 266
Db 18 CCCCTGCTACGA 7

RESULT 117
US-10-271-887-172
; Sequence 172, Application US/10271887
```

Publication No. US20030087871A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/10/271,987
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/659,845A
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 172
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-271-887-172

Query Match 2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGAGGAGGATT 32
|||||
DB 5 CCGAGGAGGATT 16

RESULT 118
US-10-003-354-41/c
; Sequence 41, Application US/10003354
; Publication No. US20030114400A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
; FILE REFERENCE: RTS-0348
; CURRENT APPLICATION NUMBER: US/10/003,354
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-354-41

Query Match 2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACAGCTCTTGA 16
|||||
DB 12 ACAGCTCTTGA 1

RESULT 119
US-10-006-883A-76/c
; Sequence 76, Application US/10006883A
; Publication No. US20030119767A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION
; FILE REFERENCE: RTS-0337
; CURRENT APPLICATION NUMBER: US/10/006,883A
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-883A-76

Query Match 2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TTTGGGACTTTG 596
|||||
DB 16 TTTGGGACTTTG 5

RESULT 120
US-10-008-789-89
; Sequence 89, Application US/10008789
; Publication No. US20030125276A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6 EX
; FILE REFERENCE: RTS-0333
; CURRENT APPLICATION NUMBER: US/10/008,789
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-008-789-89

Query Match 2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGCT 262
|||||
DB 4 GGAGCCCTGCT 15

RESULT 121
US-10-321-555-6
; Sequence 6, Application US/10321555
; Publication No. US20030134315A1
; GENERAL INFORMATION:
; APPLICANT: Warenus, Hilmar Meek
; APPLICANT: Seabra, Laurence Anthony
; TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED U
; TITLE OF INVENTION: EXPRESSION OF NEGATIVE AND POSITIVE SIGNAL TRANSDUCTION FACTORS
; FILE REFERENCE: 1417-188
; CURRENT APPLICATION NUMBER: US/10/321,555
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US/09/622,277
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00500
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: GB 9903035.5
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: GB 9814545.1
; PRIOR FILING DATE: 1998-07-03
; PRIOR APPLICATION NUMBER: GB 9812151.0
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9803447.3
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: GB 9803446.5
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR and DNA sequencing primer for exon 5 antisense
US-10-321-555-6

Query Match      2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20

RESULT 122
US-10-084-839-3772
; Sequence 3772, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPO
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3772
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3772

Query Match      2.0%; Score 12; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 TTTTACTGCTGG 444
Db 4 TTTTACTGCTGG 15

RESULT 123
US-10-448-836-61
; Sequence 61, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min

```

```

; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: oligonucleotide for detection and identification of Mycobacteri
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,836
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium vaccae
US-10-448-836-61

Query Match      2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGGCGGTG 76
Db 5 AGGTCGGCGGTG 16

RESULT 124
US-10-175-627-16/c
; Sequence 16, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; APPLICANT: Edward A. Dennis
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINAS
; FILE REFERENCE: PTS-0005
; CURRENT APPLICATION NUMBER: US/10/175,627
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-175-627-16

Query Match      2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGGCTGCACC 391
Db 12 GCGGCTGCACC 1

RESULT 125
US-10-348-073A-17/c
; Sequence 17, Application US/10348073A
; Publication No. US20030232777A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type II Beta
; TITLE OF INVENTION: Inhibitors For Inhibiting Angiogenesis
; FILE REFERENCE: ISPH-0757
; CURRENT APPLICATION NUMBER: US/10/348,073A
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 10/175,627
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-073A-17

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGGCTGCACC 391
Db 12 GCGGCTGCACC 1

RESULT 126
US-10-448-914A-61
; Sequence 61, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,914A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium vaccae
US-10-448-914A-61

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGCGCTG 76
Db 5 AGGTCGCGCTG 16

RESULT 127
```

```
US-10-178-258-37/c
; Sequence 37, Application US/10178258
; Publication No. US20030235913A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEME OXYGENASE 1 EXPRESSION
; FILE REFERENCE: HTS-0010
; CURRENT APPLICATION NUMBER: US/10/178,258
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-178-258-37

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 ACCGCAAGGCTG 364
Db 12 ACCGCAAGGCTG 1

RESULT 128
US-10-178-258-61
; Sequence 61, Application US/10178258
; Publication No. US20030235913A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEME OXYGENASE 1 EXPRESSION
; FILE REFERENCE: HTS-0010
; CURRENT APPLICATION NUMBER: US/10/178,258
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 66
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-178-258-61

Query Match          2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 ACCGCAAGGCTG 364
Db 9 ACCGCAAGGCTG 20

RESULT 129
US-10-283-443-19/c
; Sequence 19, Application US/10283443
; Publication No. US2004000580A1
; GENERAL INFORMATION:
; APPLICANT: Neo Gen Screening, Inc.
; TITLE OF INVENTION: Detecting Mutations in the GALT Gene by DNA Melting Curve Analysis
; FILE REFERENCE: 2144
; CURRENT APPLICATION NUMBER: US/10/283,443
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-443-19

Query Match          2.0%; Score 12; DB 15; Length 20;
```



```
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 GAGCCCTCTGCTA 263
Db 17 GAGCCCTCTGCTA 6

RESULT 130
US-10-349-143-11732/c
; Sequence 11732, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11732
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20_
; OTHER INFORMATION: downstream amplification primer 99-4029 for SEQ 3867, in complem
US-10-349-143-11732

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 CGTCTCTCCAGA 522
Db 14 CGTCTCTCCAGA 3

RESULT 131
US-10-289-762-1338
; Sequence 1338, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; FILE REFERENCE: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1338
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1338

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CTGAGGATCTTC 327
Db 316 CTGAGGATCTTC 327

RESULT 132
US-10-352-179-69/c
; Sequence 69, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl
; FILE REFERENCE: 22727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Oryza minuta
US-10-352-179-69

Query Match 2.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 TCCTCCGCTACA 193
Db 18 TCCTCCGCTACA 7

RESULT 133
US-10-210-290-65/c
; Sequence 65, Application US/10210290
; Publication No. US20040023378A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Eric G. Marcussen
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,290
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-65

Query Match 2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 GCGCGGCTGCA 389
Db 16 GCGCGGCTGCA 5

RESULT 134
US-10-210-479-17/c
; Sequence 17, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
```

```

; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-17

Query Match      2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      375 GCTGCGGCGGCT 386
Db      18 GCTGCGGCGGCT 7

RESULT 135
US-10-210-479-91
; Sequence 91, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-210-479-91

Query Match      2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      375 GCTGCGGCGGCT 386
Db      3 GCTGCGGCGGCT 14

RESULT 136
US-10-444-206-14
; Sequence 14, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-198

Query Match      2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      247 TCCTGGAGCCCC 258
Db      5 TCCTGGAGCCCC 16

RESULT 138
US-10-100-957A-69/c
; Sequence 69, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-6

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-14

Query Match      2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      247 TCCTGGAGCCCC 258
Db      6 TCCTGGAGCCCC 17

RESULT 137
US-10-444-206-198
; Sequence 198, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karrias, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-198

Query Match      2.0%; Score 12; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      247 TCCTGGAGCCCC 258
Db      5 TCCTGGAGCCCC 16

RESULT 138
US-10-100-957A-69/c
; Sequence 69, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-6

```

; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-69

Query Match 1.8%; Score 11; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCTGT 348
|||||
Db 11 TCTACTTCTGT 1

RESULT 139

US-10-091-281-187/c
; Sequence 187, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 187
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative BTSP/GABP.01 motif
US-10-091-281-187

Query Match 1.8%; Score 11; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 GCTCTTCTCTCC 187
|||||
Db 11 GCTCTTCTCTCC 1

RESULT 140

US-08-591-486B-97
; Sequence 97, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg F
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA: PCT/EP94/02218
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-591-486B-97

Query Match 1.8%; Score 11; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 TCATGACCTTC 423
|||||
Db 2 TCATGACCTTC 12

RESULT 141

US-09-504-231A-1366
; Sequence 1366, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1366
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1366

Query Match 1.8%; Score 11; DB 9; Length 14;
Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 216 TGGCCGCTGCT 226
:|||||:
Db 1 UGGCCGCTGCT 11

RESULT 142

US-09-274-553D-1366

; Sequence 1366, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: fpi 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 1366

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-1366

Query Match

Best Local Similarity 72.7%; Score 11; DB 9; Length 14;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy

216 TGGCGCGTGT 226

:|||||:

1 UGGCGCGUCU 11

RESULT 143

US-10-108-714-1

; Sequence 1, Application US/10108714

; Publication No. US20020128445A1

; GENERAL INFORMATION:

; APPLICANT: Regan, John W.

; APPLICANT: Gil, Daniel W.

; APPLICANT: Woodward, David F.

; TITLE OF INVENTION: No. US20020128445A1el Human Prostaglandin EP Receptor

; FILE REFERENCE: 17023 DIV CIP

; CURRENT APPLICATION NUMBER: US/10/108,714

; CURRENT FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431

; PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-108-714-1

Query Match

Best Local Similarity 100.0%; Score 11; DB 13; Length 14;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

246 CTCCTGGAGCC 256

|||||:

3 CTCCTGGAGCC 13

RESULT 144

US-09-504-231A-55/c

; Sequence 55, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: fpi 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 55

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-55

Query Match

Best Local Similarity 100.0%; Score 11; DB 9; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

359 AGGCTGAGCCC 369

|||||:

13 AGGCTGAGCCC 3

RESULT 145

US-09-504-231A-610

; Sequence 610, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: fpi 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; CURRENT FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 610

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-610

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 57 CTGGGCTAAGG 67
Db 1 CUGGGCUAAGG 11

RESULT 146
US-09-274-553D-55/c
; Sequence 55, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: FDI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-55

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
Db 13 AGGCTGAGCCC 3

RESULT 147
US-09-274-553D-610
; Sequence 610, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: FDI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
```

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; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 610
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-610

Query Match      1.8%; Score 11; DB 9; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 57 CTGGGCTAAGG 67
Db 1 CUGGGCUAAGG 11

RESULT 148
US-09-918-728B-13/c
; Sequence 13, Application US/09918728B
; Publication No. US20030105308A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleoside Triphosphates and Their Incorporation into Oligonucle
; FILE REFERENCE: MHB00-831-H (400/033)
; CURRENT APPLICATION NUMBER: US/09/918,728B
; CURRENT FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-918-728B-13

Query Match      1.8%; Score 11; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTTACCGCGC 334
Db 11 CTTACCGCGC 1

RESULT 149
US-09-918-728B-14/c
; Sequence 14, Application US/09918728B
; Publication No. US20030105308A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leonid
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleoside Triphosphates and Their Incorporation into Oligonucle
; FILE REFERENCE: MHB00-831-H (400/033)
; CURRENT APPLICATION NUMBER: US/09/918,728B
; CURRENT FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-918-728B-14

Query Match      1.8%; Score 11; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGACCGCGC 395
```

Db 11 CTGACCGCGC 1
|||||

RESULT 150

US-09-793-146-32/c

; Sequence 32, Application US/09793146

; Publication No. US20030203359A1

; GENERAL INFORMATION:

; APPLICANT: UHLMANN, EUGEN

; APPLICANT: BREIPOHL, GERHARD

; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR

; TITLE OF INVENTION: PREPARATION AND USE

; FILE REFERENCE: 02481.1437-02

; CURRENT APPLICATION NUMBER: US/09/793,146

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: P 44 08 528.1

; PRIOR FILING DATE: 1994-03-14

; PRIOR APPLICATION NUMBER: 08/402,838

; PRIOR FILING DATE: 1995-03-13

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA

US-09-793-146-32

Query Match

Best Local Similarity 1.8%; Score 11; DB 11; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 CCTGGAGCCCC 258

Db 11 CCTGGAGCCCC 1
|||||

RESULT 151

US-10-287-919-1850

; Sequence 1850, Application US/10287919

; Publication No. US20030085830A1

; GENERAL INFORMATION:

; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

; TITLE OF INVENTION: Methanococcus jannaschii complete genome.

; FILE REFERENCE: Jim Zenger Law Offices - 703-684-8333

; CURRENT APPLICATION NUMBER: US/10/287,919

; CURRENT FILING DATE: 2002-11-05

; NUMBER OF SEQ ID NOS: 2706

; SOFTWARE: Proprietary

; SEQ ID NO 1850

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Methanococcus jannaschii complete genome.

; FEATURE:

; LOCATION: (1074273)...(1074288)

; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2348

US-10-287-919-1850

Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 553 GAGGTTTCATGA 563

Db 4 GAGGTTTCATGA 14
|||||

RESULT 152

US-10-156-306-7865

; Sequence 7865, Application US/10156306

; Publication No. US20030119017A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat

; TITLE OF INVENTION: Levels of IKK-Gamma and PKR

; FILE REFERENCE: MEHB01-664-A (400/050)

; CURRENT APPLICATION NUMBER: US/10/156,306

; CURRENT FILING DATE: 2002-05-28

; NUMBER OF SEQ ID NOS: 8013

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7865

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-156-306-7865

Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 177 GCTCTTCCTCC 187

Db 5 GCUCUCCUCC 15
|||

RESULT 153

US-10-292-198-64/c

; Sequence 64, Application US/10292198

; Publication No. US20030157654A1

; GENERAL INFORMATION:

; APPLICANT: SHEN, Ben

; APPLICANT: LIU, Wen

; TITLE OF INVENTION: BIOSYTHESIS OF ENEDIYNE COMPOUNDS BY MANIPULATION OF C-1027 GENE

; TITLE OF INVENTION: PATHWAY

; FILE REFERENCE: 054030-0007

; CURRENT APPLICATION NUMBER: US/10/292,198

; CURRENT FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: US 10/159,257

; PRIOR FILING DATE: 2002-05-31

; PRIOR APPLICATION NUMBER: US 09/478,188

; PRIOR FILING DATE: 2000-01-05

; PRIOR APPLICATION NUMBER: US 60/115,434

; PRIOR FILING DATE: 1999-01-06

; NUMBER OF SEQ ID NOS: 146

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 64

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Streptomyces globisporus

US-10-292-198-64

Query Match

Best Local Similarity 1.8%; Score 11; DB 14; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 241 TTCACCTCCTG 251

Db 12 TTCACCTCCTG 2
|||||

RESULT 154

US-10-084-839-3873

; Sequence 3873, Application US/10084839

; Publication No. US20030186238A1

; GENERAL INFORMATION:

; APPLICANT: Third Wave Technologies

; APPLICANT: Allawi, Hatim

; APPLICANT: Argue, Brad T.

; APPLICANT: Bartholomay, Christian T.

; APPLICANT: Chenak, JoAnne

; APPLICANT: Curtis, Michelle L.

; APPLICANT: Eis, Peggy S.

; APPLICANT: Hall, Jeff G.

; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamachev, Victor
; APPLICANT: Lyamacheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3873
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3873

Query Match 1.8%; Score 11; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 TGAGCCCGAGG 373
|||||
DB 1 TGAGCCCGAGG 11

RESULT 155
US-10-091-281-3/c
; Sequence 3, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative OCTB/TST1.01 motif
US-10-091-281-3

Query Match 1.8%; Score 11; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GTGGAATTGCT 179
|||||
DB 12 GTGGAATTGCT 2

RESULT 156
US-10-440-850-313
; Sequence 313, Application US/10440850

; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rev
; FILE REFERENCE: 250/130 (MHB00-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,850
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 313
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-440-850-313

Query Match 1.8%; Score 11; DB 15; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAAGA 428
|||||
DB 4 ACCUCAAAGA 14

RESULT 157
US-10-440-850-314
; Sequence 314, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Rev
; FILE REFERENCE: 250/130 (MHB00-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,850
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 314
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-440-850-314

Query Match 1.8%; Score 11; DB 15; Length 15;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAAGA 428
|||||
DB 3 ACCUCAAAGA 13

RESULT 158

US-10-440-850-767
; Sequence 767, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Induction of Graft Tolerance and Reversal
; TITLE OF INVENTION: Immune Responses
; FILE REFERENCE: 250/130 (MEH00-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,850
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2285
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 767
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-440-850-767

Query Match 1.8%; Score 11; DB 15; Length 15;

Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATCAAAAT 51

Db 5 AAUCAAAT 15

RESULT 159

US-10-453-792-20/c
; Sequence 20, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4

FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-453-792-20

Query Match 1.8%; Score 11; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 ACTGCTGAAT 447

Db 13 ACTGCTGAAT 3

RESULT 160

US-09-866-108-932
; Sequence 932, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensteng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEONICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,697
; PRIOR FILING DATE: 2000-09-21

US-09-866-108-935
 ; Sequence 935, Application US/09866108
 ; Patent No. US20020048800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 60/266,860
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 15752
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; SEQ ID NO 935
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108-935

Query Match 1.8%; Score 11; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 AGGCTGAGCCC 369
 |||||
 Db 4 AGGCTGAGCCC 14

RESULT 164
 US-09-866-108-936
 ; Sequence 936, Application US/09866108
 ; Patent No. US20020048800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 60/266,860
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 15752
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; SEQ ID NO 936
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108-936

Query Match 1.8%; Score 11; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 AGGCTGAGCCC 369
 |||||
 Db 3 AGGCTGAGCCC 13

RESULT 165
 US-09-866-108-937
 ; Sequence 937, Application US/09866108
 ; Patent No. US20020048800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359

```
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 937
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-937
```

```
Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 359 AGGCTGAGCCC 369
Db 2 AGGCTGAGCCC 12
```

```
RESULT 166
US-09-866-108-938
; Sequence 938, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 938
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-938
```

```
Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 359 AGGCTGAGCCC 369
Db 1 AGGCTGAGCCC 11
```

```
RESULT 167
US-09-866-108-1462
; Sequence 1462, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1462
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1462

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCTGGGAAGG 492
|||||
Db 7 CCTGGGAAGG 17

RESULT 168
US-09-866-108-1463
; Sequence 1463, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1463
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-866-108-1463

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCTGGGAAGG 492
|||||
Db 6 CCTGGGAAGG 16

RESULT 169
US-09-866-108-1464
; Sequence 1464, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1464
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1464

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCTGGGAAGG 492
|||||
Db 7 CCTGGGAAGG 17

RESULT 168
US-09-866-108-1463
; Sequence 1463, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1463
; LENGTH: 17
; TYPE: DNA

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCTGGGAAGG 492
|||||
Db 5 CCTGGGAAGG 15

RESULT 170

US-09-866-108-1465
; Sequence 1465, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1465
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1465

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492

Db 4 CCTGGGAAGGG 14
|||||

RESULT 171

US-09-866-108-1466
; Sequence 1466, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1466
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1466

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492

Db 3 CCTGGGAAGGG 13
|||||

RESULT 172

US-09-866-108-1467
; Sequence 1467, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1467

```

```

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 482 CCTGGGAAGGG 492
Db 2 CCTGGGAAGGG 12

```

```

RESULT 173
US-09-866-108-1468
; Sequence 1468, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1468
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1468

```

```

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 482 CCTGGGAAGGG 492
Db 1 CCTGGGAAGGG 11

```

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RESULT 174
US-09-866-108-7363
; Sequence 7363, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7363
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7363

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGT 509
|||||
Db 7 GAAATTCAGT 17

RESULT 175

US-09-866-108-7370
; Sequence 7370, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 7370
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7370

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTCAGTT 510
|||||
Db 1 AAAATTCAGTT 11

RESULT 176

US-09-866-108-9635/c
; Sequence 9635, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9635
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9635

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188
|||||
Db 17 CTCCTCTCCG 7

RESULT 177

US-09-866-108-9636/c
; Sequence 9636, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 9636

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-9636

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188
|||||
Db 16 CTCCTCTCCG 6

RESULT 178

US-09-866-108-9637/c
; Sequence 9637, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 9637

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-9637

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188
|||||
Db 15 CTCCTCTCCG 5

RESULT 179

US-09-866-108-9638/c
; Sequence 9638, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108


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/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecmica Sequence Listing Engine
/ SEQ ID NO 9638
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108-9638
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Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 178 CTCCTCTCTCCG 188
DB 14 CTCCTCTCTCCG 4
```

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RESULT 180
US-09-866-108-9639/c
/ Sequence 9639, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: Aecmica Sequence Listing Engine
/ SEQ ID NO 9639
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-866-108-9639
```

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Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 178 CTCCTCTCTCCG 188
DB 13 CTCCTCTCTCCG 3
```

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RESULT 181
US-09-866-108-9640/c
/ Sequence 9640, Application US/09866108
/ Patent No. US20020048800A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AECMICA-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 9640
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9640

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCTTCTCTCCG 188
| | | | | | | | | | | | | | | | | | | | | |
Db 12 CTCTTCTCTCCG 2

RESULT 182

US-09-866-108-9641/c
; Sequence 9641, Application US/09866108
; Patent No. US20020049800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 9641
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9641

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCTTCTCTCCG 188
| | | | | | | | | | | | | | | | | | | | | |
Db 11 CTCTTCTCTCCG 1

RESULT 183

US-09-827-998-183
; Sequence 183, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 183
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-183

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 AGATTATTTT 436
| | | | | | | | | | | | | | | | | | | | | |
Db 7 AGATTATTTT 17

RESULT 184

US-09-827-998-184
; Sequence 184, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 184
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-184

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Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 6 AGATTATTTT 16

RESULT 185
US-09-827-998-185
; Sequence 185, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-185

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 5 AGATTATTTT 15

RESULT 186
US-09-827-998-186
; Sequence 186, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 186
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-186

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 4 AGATTATTTT 14

RESULT 187
US-09-827-998-187
; Sequence 187, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 187
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-187

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 3 AGATTATTTT 13

RESULT 188
US-09-827-998-188
; Sequence 188, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 188
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-188

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
  |||||
Db 2 AGATTATTTT 12

RESULT 189
US-09-827-998-189
; Sequence 189, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
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; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 189
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-189

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTATTT 436
|||||
DB 1 AGATTATTATTT 11

RESULT 190
US-09-827-998-345
; Sequence 345, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 345
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-345

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
|||||
DB 7 AAGATTATTTT 17

RESULT 191
US-09-827-998-346
; Sequence 346, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 346

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-346

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
|||||
DB 6 AAGATTATTTT 16

RESULT 192
US-09-827-998-347
; Sequence 347, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 347
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-347

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
|||||
DB 5 AAGATTATTTT 15

RESULT 193
US-09-827-998-348
; Sequence 348, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 348
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-348

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      425 AAGATTATTTT 435
Db      4 AAGATTATTTT 14

RESULT 194
US-09-827-998-349
; Sequence 349, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 349
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-349

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      425 AAGATTATTTT 435
Db      3 AAGATTATTTT 13

RESULT 195
US-09-827-998-350
; Sequence 350, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 350
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-350

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      425 AAGATTATTTT 435
Db      2 AAGATTATTTT 12

RESULT 196
US-09-827-998-351
; Sequence 351, Application US/09827998
; Patent No. US20020102252A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 351
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-351

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      425 AAGATTATTTT 435
Db      1 AAGATTATTTT 11

RESULT 197
US-09-827-998-648/c
; Sequence 648, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 648
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-648

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      17 CTACCTGTGCT 7

RESULT 198
US-09-827-998-649/c
; Sequence 649, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 649
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-649

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      16 CTACCTGTGCT 6

RESULT 199
US-09-827-998-650/c
; Sequence 650, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 650
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-650

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      15 CTACCTGTGCT 5

RESULT 200
US-09-827-998-651/c
; Sequence 651, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 651
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-651

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      12 CTACCTGTGCT 2

RESULT 201
US-09-827-998-652/c
; Sequence 652, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 652
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-652

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      13 CTACCTGTGCT 3

RESULT 202
US-09-827-998-653/c
; Sequence 653, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 653
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-653

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
Db      12 CTACCTGTGCT 2
```

RESULT 203
US-09-827-998-654/c
; Sequence 654, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMWRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 654
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-654

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

Qy 81 CTACCTGTGCT 91
|||||
Db 11 CTACCTGTGCT 1

RESULT 204
US-09-872-462-46
; Sequence 46, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 46
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-46

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

Qy 172 GAATTGCTCTT 182
|||||
Db 7 GAATTGCTCTT 17

RESULT 205
US-09-872-462-47
; Sequence 47, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 47
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-47

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

Qy 172 GAATTGCTCTT 182
|||||
Db 6 GAATTGCTCTT 16

RESULT 206
US-09-872-462-48
; Sequence 48, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

```
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 48
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-48

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      172 GAATTGCTCTT 182
Db      5 GAATTGCTCTT 15

RESULT 207
US-09-872-462-49
; Sequence 49, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 50
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-50

Query Match      1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      172 GAATTGCTCTT 182
Db      3 GAATTGCTCTT 13

RESULT 209
US-09-872-462-51
; Sequence 51, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
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; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-51

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GAATTGCTCTT 182
||| |||||
Db 2 GAATTGCTCTT 12

RESULT 210
US-09-872-462-52
; Sequence 52, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AECOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 52
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-52

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 GAATTGCTCTT 182
||| |||||
Db 1 GAATTGCTCTT 11

RESULT 211
US-09-864-785-224
; Sequence 224, Application US/09864785
; Patent No. US2002017568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 224
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-224

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GCTGCGCGGC 385
||| |||||
Db 7 GCUGCGCGGC 17

RESULT 212
US-09-864-785-622
; Sequence 622, Application US/09864785
; Patent No. US2002017568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 622
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-864-785-622

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553
|||||:|:|:
Db 7 GCCCCUGAUG 17

RESULT 213

US-09-864-785-623
; Sequence 623, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 623
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-623

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553
|||||:|:|:
Db 6 GCCCCUGAUG 16

RESULT 214

US-09-864-785-624
; Sequence 624, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 624
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-624

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553

Db 5 GCCCCUGAUG 15
|||||:|:|:

RESULT 215

US-09-864-785-625
; Sequence 625, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 625
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-625

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553
|||||:|:|:
Db 4 GCCCCUGAUG 14

RESULT 216

US-09-864-785-1528
; Sequence 1528, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1528
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1528

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGGC 385
|||||:|:|:
Db 6 GCUGCGCGGC 16

RESULT 217

US-09-864-785-1529
; Sequence 1529, Application US/09864785

Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1529
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1529

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385
|||:|||||
Db 3 GCUGCGCGCGC 13

RESULT 218
US-09-864-785-1671
; Sequence 1671, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1671
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1671

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553
|||:|||||
Db 3 GCCCUGAUG 13

RESULT 219
US-09-864-785-2135
; Sequence 2135, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2135
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2135

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 72.7%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 543 GCCCCTGTATG 553
|||:|||||
Db 1 GCCCUGAUG 11

RESULT 220
US-09-864-785-2779
; Sequence 2779, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2779
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2779

Query Match 1.8%; Score 11; DB 9; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385
|||:|||||
Db 4 GCUGCGCGCGC 14

RESULT 221
US-09-864-785-2780
; Sequence 2780, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2780

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; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2780

Query Match
Best Local Similarity 1.8%; Score 11; DB 9; Length 17;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385
Db 1 GCUGCGCGCGC 11

RESULT 222
US-09-825-805-591/c
; Sequence 591, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1998-11-04
; PRIOR FILING DATE: 1998-04-29
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 591
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-591

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGA 253
Db 11 CACCTCCTGGA 1

RESULT 223
US-09-825-805-699/c
; Sequence 699, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
```

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; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 1999-12-30
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1999-12-29
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1998-11-04
; PRIOR FILING DATE: 1998-04-29
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 699
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-699

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGTC 261
Db 13 GGAGCCCTGTC 3

RESULT 224
US-09-730-289B-165
; Sequence 165, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MHB00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 165
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-165

Query Match
Best Local Similarity 1.8%; Score 11; DB 10; Length 17;
Matches 4; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTTAC 438
Db 7 AUAUUUUUAC 17

RESULT 225
US-09-730-289B-171
; Sequence 171, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MEH800-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 171
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-730-289B-171

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 27.3%; Pred. No. 2.3e+05;
Matches 3; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTTACT 439
Db 1 UUAUUUUJACU 11

RESULT 226
US-09-818-875-931
; Sequence 931, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-931

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 GAGGGAACCCC 306
Db 2 GAGGGAACCCC 12

RESULT 227
US-09-818-875-932/c
; Sequence 932, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single

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; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-932

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 296 GAGGGAACCCC 306
Db 16 GAGGGAACCCC 6

RESULT 228
US-09-818-875-3798
; Sequence 3798, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3798
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-3798

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 291 TCTCGAGGGA 301
Db 4 TCTCGAGGGA 14

RESULT 229
US-09-818-875-3795/c
; Sequence 3799, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.

```

```

; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3799
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-3799

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Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 291 TCTGCGGAGGA 301
      |||||
DB 14 TCTGCGGAGGA 4

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RESULT 230
US-09-780-533A-52/c
; Sequence 52, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haebelri, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MSHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 52
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-52

```

```

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 362 CTGAGCCCGAG 372
      |||||
DB 11 CTGAGCCCGAG 1

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```

RESULT 231
US-09-780-533A-57
; Sequence 57, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim

```

```

; APPLICANT: Chowrira, Bharat
; APPLICANT: Haebelri, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MSHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 57
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-57

```

```

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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QY 175 TTGCTCTTCCT 185
      ::|||::|:
DB 4 UUGCUCUCCU 14

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RESULT 232
US-09-780-533A-58
; Sequence 58, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haebelri, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MSHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 58
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-58

```

```

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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```

QY 175 TTGCTCTTCCT 185
      ::|||::|:
DB 2 UUGCUCUCCU 12

```

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RESULT 233
US-09-780-533A-59
; Sequence 59, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haebelri, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MSHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797

```

```
/ PRIOR FILING DATE: 2000-02-11
/ NUMBER OF SEQ ID NOS: 6679
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 59
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-09-780-533A-59

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCT 185
DB 1 UUGUCUUCUU 11

RESULT 234
US-09-780-533A-943/c
; Sequence 943, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 943
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-943

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGC 261
DB 17 GGAGCCCTGC 7

RESULT 235
US-09-780-533A-944/c
; Sequence 944, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 944
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-09-966-880a-7_copy_80_676.Oligo.rnpb

US-09-780-533A-944

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTGC 261
DB 11 GGAGCCCTGC 1

RESULT 236
US-09-780-533A-946/c
; Sequence 946, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 946
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-946

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 TGAGCCCGAGG 373
DB 17 TGAGCCCGAGG 7

RESULT 237
US-09-780-533A-952
; Sequence 952, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 952
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-952

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+05;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCT 185
```

DB	5	UUGCUCUCCU 15	1.8%; Score 11; DB 10; Length 17; Best Local Similarity 45.5%; Pred. No. 2.3e+05; Mismatches 6; Conservative 0; Indels 0; Gaps 0;
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	
Db	3	UUGCUCUCCU 13	
Qy	3	UUGCUCUCCU 13	
Db	175	TTGCTCTTCTCT 185	
Qy	175	TTGCTCTTCTCT 185	


```

; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2418
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2418

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCCCTGC 261
    |||||
Db 15 GGAGCCCCCTGC 5

RESULT 243
US-09-780-533A-2419/c
; Sequence 2419, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2419
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2419

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCCCTGC 261
    |||||
Db 14 GGAGCCCCCTGC 4

RESULT 244
US-09-848-754A-921/c
; Sequence 921, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 921
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

```

```

US-09-848-754A-921

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTCGA 253
    |||||
Db 17 CACCTCCTCGA 7

RESULT 245
US-09-848-754A-922/c
; Sequence 922, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 922
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-922

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTCGA 253
    |||||
Db 16 CACCTCCTCGA 6

RESULT 246
US-09-848-754A-2178/c
; Sequence 2178, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2178
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2178

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTCGA 253
    |||||
Db 11 CACCTCCTCGA 1

RESULT 247
US-09-848-754A-3135/c
; Sequence 3135, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

```

;; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
;; FILE REFERENCE: MEHB00-958-I (400/018)
;; CURRENT FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: US 09/848,754A
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 3135
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-848-754A-3135

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCTCTGGA 253
DB 15 CACCTCTCTGGA 5

RESULT 248
US-09-848-754A-3136/c
;; Sequence 3136, Application US/09848754A
;; Publication No. US20030073207A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
;; FILE REFERENCE: MEHB00-958-I (400/018)
;; CURRENT FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: US/09/848,754A
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 3136
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-848-754A-3136

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCTCTGGA 253
DB 14 CACCTCTCTGGA 4

RESULT 249
US-09-848-754A-3137/c
;; Sequence 3137, Application US/09848754A
;; Publication No. US20030073207A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
;; FILE REFERENCE: MEHB00-958-I (400/018)
;; CURRENT FILING DATE: 2001-05-03
;; PRIOR APPLICATION NUMBER: US/09/848,754A
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 3137
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-848-754A-3137

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCTCTGGA 253
DB 12 CACCTCTCTGGA 2

RESULT 250
US-09-776-474-201/c
;; Sequence 201, Application US/09776474
;; Publication No. US20030087847A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: Jarvis, Thale
;; APPLICANT: Boher, Robert
;; APPLICANT: Holman, Patricia
;; APPLICANT: Fattaey, Ali
;; APPLICANT: McSwiggen, Jim
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
;; FILE REFERENCE: MEHB00-955-A (400/008)
;; CURRENT FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: US 60/179,983
;; PRIOR FILING DATE: 2000-03-02
;; NUMBER OF SEQ ID NOS: 2992
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 201
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-201

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
DB 15 TTCTGTGAGGA 5

RESULT 251
US-09-776-474-205
;; Sequence 205, Application US/09776474
;; Publication No. US20030087847A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: Jarvis, Thale
;; APPLICANT: Boher, Robert
;; APPLICANT: Holman, Patricia
;; APPLICANT: Fattaey, Ali
;; APPLICANT: McSwiggen, Jim
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
;; FILE REFERENCE: MEHB00-955-A (400/008)
;; CURRENT FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: US 60/179,983
;; PRIOR FILING DATE: 2000-03-02
;; NUMBER OF SEQ ID NOS: 2992
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 205
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-205

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCAA 42
:|:|:|:|:|
Db 7 UUCUUUACCAA 17

RESULT 252

US-09-776-474-206
; Sequence 206, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MEHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 206
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-206

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCAA 42
:|:|:|:|:|
Db 5 UUCUUUACCAA 15

RESULT 253

US-09-776-474-207
; Sequence 207, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MEHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 207
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-207

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 32 TTCTTTACCAA 42
:|:|:|:|:|
Db 4 UUCUUUACCAA 14

RESULT 254

US-09-776-474-208
; Sequence 208, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CK)
; FILE REFERENCE: MEHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 208
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-208

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCAA 42
:|:|:|:|:|
Db 3 UUCUUUACCAA 13

RESULT 255

US-09-776-474-571/C
; Sequence 571, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CK)
; FILE REFERENCE: MEHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 571
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-571

Query Match 1.8%; Score 11; DB 10; Length 17;

```
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
  |||||
Db 17 TTCTGTGAGGA 7

RESULT 256
US-09-776-474-572/c
; Sequence 572, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 572
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-572

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
  |||||
Db 16 TTCTGTGAGGA 6

RESULT 257
US-09-776-474-573/c
; Sequence 573, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 573
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-573
```

```
Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
  |||||
Db 14 TTCTGTGAGGA 4

RESULT 258
US-09-776-474-574/c
; Sequence 574, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 574
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-574

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
  |||||
Db 12 TTCTGTGAGGA 2

RESULT 259
US-09-776-474-582
; Sequence 582, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 582
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-582
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Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCA 42
Db 6 UUCUUUACCA 16

RESULT 260
US-09-776-474-583
; Sequence 583, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Pattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MEH800-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-583

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 54.5%; Pred. No. 2.3e+05;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTCTTTACCA 42
Db 1 UUCUUUACCA 11

RESULT 261
US-09-776-474-1146/c
; Sequence 1146, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Pattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MEH800-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1146
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

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US-09-776-474-1146

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGAGGA 353
Db 11 TTCTGTGAGGA 1

RESULT 262
US-09-930-423-478
; Sequence 478, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MEH800.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-478

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382
Db 4 GGGGCTGCGGC 14

RESULT 263
US-09-930-423-1012
; Sequence 1012, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MEH800.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1012

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382
Db 3 GGGGCTGCGGC 13

RESULT 264
US-09-930-423-1199
; Sequence 1199, Application US/09930423
; Publication No. US20030092003A1

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; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1199
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1199

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382
Db 6 GGGGCTGCGGC 16

RESULT 265
US-09-930-423-1533
; Sequence 1533, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1533
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1533

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382
Db 7 GGGGCTGCGGC 17

RESULT 266
US-09-930-423-1534
; Sequence 1534, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1534
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1534

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Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGGC 382
Db 1 GGGGCTGCGGC 11

RESULT 267
US-09-780-164-723/c
; Sequence 723, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-723

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGTTCGTCTCT 517
Db 13 AGTTCGTCTCT 3

RESULT 268
US-09-780-164-911/c
; Sequence 911, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 911
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-911

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGTTCGTCTCT 517
Db 15 AGTTCGTCTCT 5

RESULT 269

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```

US-09-780-164-912/c
; Sequence 912, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; CURRENT APPLICATION NUMBER: US/09/780,164
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 912
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-912

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGTTCGTCTCT 517
Db 11 AGTTCGTCTCT 1

RESULT 270
US-09-780-164-1049/c
; Sequence 1049, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; CURRENT APPLICATION NUMBER: US/09/780,164
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1049
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-1049

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 AGTTCGTCTCT 517
Db 15 AGTTCGTCTCT 6

RESULT 271
US-09-827-395A-19
; Sequence 19, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowhira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MEH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11

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; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-19

Query Match
Best Local Similarity 81.8%; Score 11; DB 10; Length 17;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 6 CCUCCUGGAGC 16

RESULT 272
US-09-827-395A-195
; Sequence 195, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowhira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MEH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 195
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-195

Query Match
Best Local Similarity 81.8%; Score 11; DB 10; Length 17;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 7 CCUCCUGGAGC 17

RESULT 273
US-09-827-395A-196
; Sequence 196, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowhira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MEH800-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11

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; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-196

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 5 CCUCUGGAGC 15

RESULT 274
US-09-827-395A-197
; Sequence 197, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-11
; PRIOR FILING DATE: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 197
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-197

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 4 CCUCUGGAGC 14

RESULT 275
US-09-827-395A-879
; Sequence 879, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 879
; LENGTH: 17
; TYPE: RNA

```

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; ORGANISM: Homo sapiens
; US-09-827-395A-879

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 3 CCUCUGGAGC 13

RESULT 276
US-09-827-395A-880
; Sequence 880, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 880
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-827-395A-880

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 245 CCTCCTGGAGC 255
Db 2 CCUCUGGAGC 12

RESULT 277
US-09-740-332-345
; Sequence 345, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
; US-09-740-332-345

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```


QY 57 CTGGGCTAAGG 67
|:||||:||||
Db 5 CUGGGCUAAGG 15

RESULT 278
US-09-740-332-916
; Sequence 916, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 916
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-916

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGGGCGGCT 386
|:|||||||||:
Db 7 CUGGGCGGCU 17

RESULT 279
US-09-740-332-917
; Sequence 917, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 917
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-917

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGGGCGGCT 386
|:|||||||||:
Db 4 CUGGGCGGCU 14

RESULT 280
US-09-740-332-918
; Sequence 918, Application US/09740332
; Publication No. US20030125270A1

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 918
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-918

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGGGCGGCT 386
|:|||||||||:
Db 1 CUGGGCGGCU 11

RESULT 281
US-09-740-332-3638/c
; Sequence 3638, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3638
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3638

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 CTGGGGCGGCT 386
|:|||||||||:
Db 15 CTGGGGCGGCT 5

RESULT 282
US-09-740-332-3639/c
; Sequence 3639, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0

US-09-740-332-4210-122

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 376 CTGGCGGGCT 386
Db 12 CTGGCGGGCT 2

RESULT 283

US-09-740-332-4210/c

Sequence 4210, Application US/09740332
Publication No. US20030125270A1

GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
FILE REFERENCE: RPI 400/003
CURRENT APPLICATION NUMBER: US/09/740,332
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9704
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4210
LENGTH: 17
TYPE: RNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION:
OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-4210

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 CTGGGCTAAGG 67
Db 14 CTGGGCTAAGG 4

RESULT 284

US-09-792-818-122

Sequence 122, Application US/09792818
Publication No. US20030134806A1

GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
FILE REFERENCE: MBHB00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO 122
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens

US-09-792-818-122

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 515 TCTCCAGACAG 525
Db 6 UCUCACAGACAG 16

RESULT 285

US-09-792-818-310

Sequence 310, Application US/09792818
Publication No. US20030134806A1

GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
FILE REFERENCE: MBHB00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO 310
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens

US-09-792-818-310

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 515 TCTCCAGACAG 525
Db 7 UCUCACAGACAG 17

RESULT 286

US-09-792-818-311

Sequence 311, Application US/09792818
Publication No. US20030134806A1

GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira
APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul
APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
FILE REFERENCE: MBHB00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304
SOFTWARE: PatentIn version 3.0
SEQ ID NO 311
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens

US-09-792-818-311

Query Match 1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 515 TCTCCAGACAG 525

US-09-792-818-518
; Sequence 518, Application US/09792818

```
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 707
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-707

Query Match          1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      15 GATGAACCGGA 25
Db      4 GAUGAACCGGA 14

RESULT 292
US-09-792-818-805
; Sequence 805, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 805
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-805

Query Match          1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      515 TCTCCAGACAG 525
Db      3 UCUCACAGACAG 13

RESULT 293
US-09-792-818-835
; Sequence 835, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 835
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-835
```

```
Query Match          1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 GATGAACCGGA 25
Db      1 GAUGAACCGGA 11
```

```
RESULT 294
US-09-745-237A-478
; Sequence 478, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-478
```

```
Query Match          1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      372 GGGGCTCGGC 382
Db      4 GGGGCTCGGC 14
```

```
RESULT 295
US-09-745-237A-1012
; Sequence 1012, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1012
```

```
Query Match          1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      372 GGGGCTCGGC 382
Db      3 GGGGCTCGGC 13
```

```
RESULT 296
US-09-745-237A-1199
; Sequence 1199, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1199
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1199

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGGCGC 382
      |||||:||||
Db      6 GGGGCTGGCGC 16

RESULT 297
US-09-745-237A-1533
; Sequence 1533, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1533
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1533

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGGCGC 382
      |||||:||||
Db      7 GGGGCTGGCGC 17

RESULT 298
US-09-745-237A-1534
; Sequence 1534, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 1534
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1534

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      372 GGGGCTGGCGC 382
      |||||:||||
Db      1 GGGGCTGGCGC 11

RESULT 299
US-09-817-879-345
; Sequence 345, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 345
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-345

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      57 CTGGGCTAAGG 67
      |:|:|:|:|
Db      5 CUGGGCTAAGG 15

RESULT 300
US-09-817-879-916
; Sequence 916, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 916
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-916

Query Match      1.8%; Score 11; DB 10; Length 17;
Best Local Similarity 81.8%; Pred. No. 2.3e+05;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 376 CTGCGGGGCT 386
|:|||||:
Db 7 CUGCGGGGCU 17

Search completed: March 5, 2004, 00:28:13
Job time : 310 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 4, 2004, 21:56:12 ; Search time 2279 Seconds
(without alignments)
7822.607 Million cell updates/sec

Title: US-09-966-880A-7_COPY_80_676
Perfect score: 597
Sequence: 1 atggcagcctcttgatgaa.....ttcgtactttgggactttga 597

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0
Total number of hits satisfying chosen parameters: 8854

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_plg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	11	1.8	19 9	AI584018	ts12e10.x
2	11	1.8	19 10	AW248934	2819262.3
3	11	1.8	20 28	AZ308068	1M0010N08
4	10	1.7	19 28	AZ308665	1M0011F19

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
AI584018
LOCUS
DEFINITION
ts12e10.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2228394 3', similar to SW:PRPL_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO 1, mRNA sequence.
ACCESSION
AI584018
VERSION
AI584018.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 19)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

ALIGNMENTS

AI584018 19 bp mRNA linear EST 14-DEC-1999
ts12e10.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2228394 3', similar to SW:PRPL_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO 1, mRNA sequence.
AI584018
AI584018.1
GI:4569915
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 3996 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2228394"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 Kb. Life technologies catalog #:
11548-013"

ORIGIN
Query Match 1.8%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGCGCCG 222
Db 6 ACCCTGCGCCG 16

RESULT 2
AW248934
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW248934 19 bp mRNA linear EST 07-JAN-2000
2819262.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819262 3',
mRNA sequence.
AW248934
AW248934.1 GI:6591927
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819262.5prime
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
PHRED quality bases following vector sequence. Very low
Quality Sequence: trace file contained 19 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence; this cDNA insert was polyadenylated.
Plate: LLCM1 row: C column: 7
High quality sequence stop: 8.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819262"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"

FEATURES
source

QY 585 TTTCGGACTTT 595
Db 8 TTTCGGACTTT 18

ORIGIN
Query Match 1.8%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TTTCGGACTTT 595
Db 8 TTTCGGACTTT 18

RESULT 3
AZ308068
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ308068 20 bp DNA linear GSS 29-SEP-2000
1M0010N08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0010N08 R, genomic survey sequence.
AZ308068
AZ308068.1 GI:10347690
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: N column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0010N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

Insert Length: 3996 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2228394"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 Kb. Life technologies catalog #:
11548-013"

ORIGIN
Query Match 1.8%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGCGCCG 222
Db 6 ACCCTGCGCCG 16

RESULT 2
AW248934
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW248934 19 bp mRNA linear EST 07-JAN-2000
2819262.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819262 3',
mRNA sequence.
AW248934
AW248934.1 GI:6591927
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819262.5prime
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
PHRED quality bases following vector sequence. Very low
Quality Sequence: trace file contained 19 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence; this cDNA insert was polyadenylated.
Plate: LLCM1 row: C column: 7
High quality sequence stop: 8.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819262"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"

FEATURES
source

QY 585 TTTCGGACTTT 595
Db 8 TTTCGGACTTT 18

ORIGIN
Query Match 1.8%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 TTTCGGACTTT 595
Db 8 TTTCGGACTTT 18

RESULT 3
AZ308068
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ308068 20 bp DNA linear GSS 29-SEP-2000
1M0010N08R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0010N08 R, genomic survey sequence.
AZ308068
AZ308068.1 GI:10347690
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: N column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0010N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.8%; Score 11; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 GCTCTCTCTCC 187
|||||
Db 2 GCTCTCTCTCC 12

RESULT 4
AZ308665
LOCUS
DEFINITION IM001F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011F19 R, genomic survey sequence.

ACCESSION AZ308665
VERSION AZ308665.1 GI:10348891
KEYWORDS
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 19)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0011 row: F column: 19

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011F19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCC 184
|||||
Db 7 TTGCTCTTCC 16

RESULT 5

AZ790121

LOCUS

DEFINITION 2M0038P21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0038P21 F, genomic survey sequence.

ACCESSION AZ790121

VERSION AZ790121.1 GI:12931652

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT
Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: P column: 21

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0038P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 433 TTTTACTGCT 442
|||||
Db 5 TTTTACTGCT 14

RESULT 6

AZ804026 19 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M064007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M064007 R, genomic survey sequence.

ACCESSION AZ804026
VERSION AZ804026.1 GI:12956349
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0064 row: 0 column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M064007"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAGACT 474
|||||
Db 5 TGAAGAGACT 14

RESULT 7

AZ440002 20 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION 1M0230E19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0230E19 R, genomic survey sequence.

ACCESSION AZ440002
VERSION AZ440002.1 GI:10564015
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0230 row: E column: 19

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0230E19"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 CATGACCTTC 423
|||||||
Db 10 CATGACCTTC 19

RESULT 8
AZ611227/c
LOCUS
DEFINITION
IM0436E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0436E13 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: E column: 13

Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 ACCCCAACT 311
|||||||
Db 19 ACCCCAACT 10

RESULT 9

AZ772893

LOCUS
DEFINITION
IM0584D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0584D09 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0584 row: D column: 09

Seq primer: CGTGTAAACGACGCCACT
Class: plasmid ends

High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0584D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 478 AAAGCCTGGG 487
|||||||
Db 9 AAAGCCTGGG 18

RESULT 10

AZ815477
LOCUS 20083C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M083C17 R, genomic survey sequence.

ACCESSION AZ815477
VERSION AZ815477.1 GI:12985385
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0083 row: C column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M083C17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 GTGACAGTGC 116
|||||||
Db 1 GTGACAGTGC 10

RESULT 11

AZ964660
LOCUS 2M0234M21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0234M21 F, genomic survey sequence.

ACCESSION AZ964660
VERSION AZ964660.1 GI:13835887
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0234 row: M column: 21

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0234M21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.7%; Score 10; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCCGACT 289

Db 11 GTGGCCGACT 20

RESULT 12

CF323895

LOCUS

DEFINITION HDN--05-A22.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA sequence.

ACCESSION

CF323895

VERSION

CF323895.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 10)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..10

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDN--05-A22"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDAC1-overexpressing transgenic rice lambda

phage cDNA library II (HDN)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

ORIGIN

Query Match

1.5%; Score 9; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 GCCCGAGGG 374

Db 1 GCCCGAGGG 9

RESULT 13

BH170808/c

LOCUS

DEFINITION SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_003378, genomic survey sequence.

ACCESSION

BH170808

VERSION

BH170808.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 13)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..13

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_003378"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match

1.5%; Score 9; DB 28; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 CTTACCGC 332

Db 13 CTTACCGC 5

RESULT 14

BQ584986

LOCUS

DEFINITION BQ584986 15 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-002-K24-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION

BQ584986

VERSION

BQ584986.1

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, W., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

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and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 2 row: K column: 24
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:181716"
/db_xref="taxon:161934"
/clone="024-002-K24"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 1.5%; Score 9; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 444 GAATACCTTT 452
|||||
Db 6 GAATACCTTT 14

RESULT 15
HSM001764
ID HSM001764 standard; mRNA; EST; 16 BP.
XX AC AL037434;
XX SV AL037434.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp564O1471_s1 (from clone DKFZp564O1471)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RP 1-16
XX RA Bloecher H., Boescher M., Brandt P., Meves W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferstritz 18a D-82152 Martinsried, GERMANY

```

```

XX Clone from S. Wiemann, sequenced by GBF within the cDNA
CC sequencing consortium of the German Genome Project
CC No x1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source
FT 1. .16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp564O1471"
FT /clone_lib="564 (synonym: hbr2). Vector pAMPI; host
FT x1-2blue; sites NotI + Sali"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX SQ Sequence 16 BP; 5 A; 1 C; 0 G; 10 T; 0 other;
Query Match 1.5%; Score 9; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTTA 437
|||||
Db 3 TTATTTTA 11

RESULT 16
BQ586219/c
LOCUS
DEFINITION E012392-024-013-C19-SP6-MPiz-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-C19 5-PRIME, mRNA sequence.
ACCESSION BQ586219
VERSION BQ586219.1 GI:26115801
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Anaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 13 row: C column: 19
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186651"
/db_xref="taxon:161934"
/clone="024-013-C19"
/tissue_type="leaf"
/lab_host="EMDH10B"

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FEATURES
source

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/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Query Match 1.5%; Score 9; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TTTCTTACC 40
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DB 13 TTTCTTACC 5

RESULT 17

CF920788 16 bp mRNA linear EST 05-NOV-2003
LOCUS gmrRw3-01_E05_1_039 Soybean root hair subtracted cDNA library
DEFINITION gmrRw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF920788
VERSION CF920788.1 GI:38191582
KEYWORDS EST.
SOURCE Glycine max (soybean)

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 16)

AUTHORS Scheffler B.E., Huang, S., Liu X., Nguyen, H., Duke, M. and Stacey, G.
TITLE Expressed sequence tags from soybean root hair subtractive cDNA library

JOURNAL Unpublished (2003)

COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: stacey@missouri.edu
Single pass sequence
Seq primer: T7

FEATURES

source

1..16
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmrRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

ORIGIN

Query Match 1.5%; Score 9; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 TCTTCTCC 187
|||||

DB 3 TCTTCTCC 11

RESULT 18

AZ633696

LOCUS 17 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0489001F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0489001 F, genomic survey sequence.

ACCESSION AZ633696
VERSION AZ633696.1 GI:11755886
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 17)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

TELE: 801 585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: 0 column: 01
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 465.

FEATURES

source

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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0489001"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 TGGACTTTG 139
|||||
DB 4 TGGACTTTG 12

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AI695637
LOCUS       we51q07.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2344668 3,
DEFINITION similar to TR:Q01944 Q01944 EXTENSIN ;contains element MER22
repetitive element ;, mRNA sequence.
ACCESSION  AI695637
VERSION     AI695637.1 GI:4983537
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL     Tumor Gene Index
COMMENT     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1738 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocytic leukemia"
                     /clone_lib="THP-1 (TIB-202)"
                     /notes="Vector: PCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO."

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      485 GGGAGGGC 493
Db      10 GGGAGGGC 18

RESULT 20
LOCUS      AW059909
DEFINITION AUTH.bsst.upc15.ba.A040e11 UPC15 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW059909
VERSION     AW059909.1 GI:6652231
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)

AI695637
LOCUS       we51q07.x1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:2344668 3,
DEFINITION similar to TR:Q01944 Q01944 EXTENSIN ;contains element MER22
repetitive element ;, mRNA sequence.
ACCESSION  AI695637
VERSION     AI695637.1 GI:4983537
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL     Tumor Gene Index
COMMENT     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1738 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     /clone_lib="THP-1 (TIB-202)"
                     /notes="Vector: PCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      485 GGGAGGGC 493
Db      10 GGGAGGGC 18

RESULT 20
LOCUS      AW059909
DEFINITION AUTH.bsst.upc15.ba.A040e11 UPC15 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW059909
VERSION     AW059909.1 GI:6652231
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 19)

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Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletz,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
20144098
MEDLINE
PUBMED
COMMENT   Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: tim@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the up-regulated gate.
High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /cell_type="monocytic leukemia"
                     /clone_lib="THP-1 (TIB-202)"
                     /notes="Vector: PCR2.1; Cloning of PCR products from
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                     cells induced with 100 nM PMA in DMSO."

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      583 ACTTTGGGA 591
Db      3 ACTTTGGGA 11

RESULT 21
LOCUS      BM399684
DEFINITION 5009-0-60-A01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM399684
VERSION     BM399684.1 GI:18199737
KEYWORDS   EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT     Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..19
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                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)

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ORIGIN
Query Match      1.5%; Score 9; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 GCTGAGCCC 369
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Db 2 GCTGAGCCC 10

RESULT 22
CF276582/c
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL--01-M14, mRNA sequence.
ACCESSION
CF276582
VERSION
CF276582.1 GI:33653968
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza sativa
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--03-C08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      1.5%; Score 9; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 ATTCAAAAA 50
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Db 19 ATTCAAAAA 11

RESULT 24
A2309116
LOCUS
DEFINITION
IM0012E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0012B23 R, genomic survey sequence.
ACCESSION
A2309116
VERSION
A2309116.1 GI:10349784
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 GCTGAGCCC 369
    |||||
Db 2 GCTGAGCCC 10

RESULT 22
CF276582/c
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL--01-M14, mRNA sequence.
ACCESSION
CF276582
VERSION
CF276582.1 GI:33653968
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza sativa
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      1.5%; Score 9; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 ACTGTGCT 91
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Db 18 ACTGTGCT 10

RESULT 23
CF309636/c
LOCUS
DEFINITION
ABF--03-C08.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--03-C08, mRNA sequence.
ACCESSION
CF309636
VERSION
CF309636.1 GI:33661397
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza sativa
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--01-M14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19

FEATURES

source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0012E23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|G14732114|G14732114), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCT 346
 |||||
 Db 11 TCTACTTCT 19

RESULT 25
 AZ312945/c
 LOCUS
 DEFINITION 1M0029P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0029P03 F, genomic survey sequence.

ACCESSION AZ312945.1 GI:10357381
 VERSION
 KEYWORDS
 SOURCE

Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center

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 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0029 row: P column: 03

Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19

FEATURES

source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0029P03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|G14732114|G14732114), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 TGTAGAAAA 461
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 Db 9 TGTAGAAAA 1

RESULT 26
 AZ323590
 LOCUS
 DEFINITION 1M0045A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0045A07 F, genomic survey sequence.

ACCESSION AZ323590
 VERSION
 KEYWORDS
 SOURCE

Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center

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 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: A column: 07

Seq primer: CGTTGTAATAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0045A07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 528 TCGGGCGCAT 536
 |||||
 Db 4 TCGGGCGCAT 12

RESULT 27
 AZ329996/c
 LOCUS
 DEFINITION
 1M0054L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0054L10 R, genomic survey sequence.

ACCESSION
 VERSION
 AZ329996.1 GI:10391268

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,I.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

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 University of Utah

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: L column: 10

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC1M0054L10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCT 442
 |||||
 Db 9 TTTACTGCT 1

RESULT 28
 AZ331628

LOCUS

DEFINITION
 1M0059M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0059M12 R, genomic survey sequence.

ACCESSION
 VERSION
 AZ331628.1 GI:10394503

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,I.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

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 University of Utah Genome Center
 University of Utah

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Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: M column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

source

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1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0059M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 437

Db 9 TTATTTT 17

RESULT 29

LOCUS

AZ344069 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M007G21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M007G21 R, genomic survey sequence.

ACCESSION

AZ344069

VERSION

AZ344069.1

GI:10422948

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: G column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

source

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1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 ACCCCAC 310

Db 3 ACCCCAC 11

RESULT 30

LOCUS

AZ345537 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080P01 F, genomic survey sequence.

ACCESSION

AZ345537

VERSION

AZ345537.1

GI:10424774

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 01

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTTATTTTA 437

Db 9 TTTATTTTA 1

RESULT 31

AZ413661

LOCUS

DEFINITION IM0197107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0197107 R, genomic survey sequence.

ACCESSION AZ413661

VERSION AZ413661.1 GI:10537590

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0197 row: I column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 AAGGGTCGG 72

Db 4 AAGGGTCGG 12

RESULT 32

AZ424757/c

LOCUS

DEFINITION IM0204G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0204G02 R, genomic survey sequence.

ACCESSION AZ424757

VERSION AZ424757.1 GI:10548770

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

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University of Utah Genome Center

University of Utah

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84112, USA

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Insert Length: 10000 Std Error: 0.00

Plate: 0204 row: G column: 02

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19
 source

FEATURES

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0204G02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ACATCCTTT 126
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 Db 18 ACATCCTTT 10

RESULT 33
 AZ579566
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0367L08P Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0367L08 F, genomic survey sequence.

ACCESSION AZ579566
 VERSION AZ579566.1 GI:11693995
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

84112, USA

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0367 row: L column: 08

Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19
 source

FEATURES

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0367L08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 547 CTGTATGAG 555
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 Db 10 CTGTATGAG 18

RESULT 34
 AZ585367/c

LOCUS

DEFINITION 1M0390D06R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0390D06 R, genomic survey sequence.

ACCESSION AZ585367
 VERSION AZ585367.1 GI:11707178
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

84112, USA

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0390 row: D column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0390D06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 411 CATCATGAC 419
|||||||

Db 9 CATCATGAC 1

RESULT 35

AZ585898

LOCUS AZ585898 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0391L02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391L22 F, genomic survey sequence.

ACCESSION AZ585898

VERSION AZ585898.1 GI:11708088

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0391 row: L column: 22

Seq primer: CGTTGTAACAGCGGCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0391L22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCT 346
|||||||

Db 6 TCTACTTCT 14

RESULT 36

AZ593103/c

LOCUS AZ593103 19 bp DNA linear GSS 13-DEC-2000

DEFINITION IM0404N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0404N24 F, genomic survey sequence.

ACCESSION AZ593103

VERSION AZ593103.1 GI:11715293

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0404 row: N column: 24

Seq primer: CGTTGTAACAGCAGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. 19

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0404N24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 ACGTGGAAAT 175

Db |||||

17 ACGTGGAAAT 9

RESULT 37

AZ595016/c

LOCUS AZ595016 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0407C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0407C19 F, genomic survey sequence.

ACCESSION AZ595016

VERSION AZ595016.1 GI:11717206

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

Mice whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: C column: 19

TITLE

Mice whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: C column: 19

Seq primer: CGTTGTAACAGCAGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. 19

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0407C19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 370 GAGGGGCTG 378

Db |||||

14 GAGGGGCTG 6

RESULT 38

AZ595098/c

LOCUS AZ595098 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0407E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0407E05 R, genomic survey sequence.

ACCESSION AZ595098

VERSION AZ595098.1 GI:11717288

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

Mice whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: E column: 05

TITLE

Mice whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: E column: 05

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19

FEATURES

source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0407E05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AAAATGTC 54
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 DB 9 AAAATGTC 1

RESULT 39
 AZ604588
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0425E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0425E04 R, genomic survey sequence.

ACCESSION AZ604588
 VERSION AZ604588.1 GI:11726778
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunn,D., Ayagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0425 row: E column: 04

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19

FEATURES

source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0425E04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAA 49
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 DB 5 AATTCAAA 13

RESULT 40
 AZ761834/c
 LOCUS 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION IM0556E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0556E19 F, genomic survey sequence.

ACCESSION AZ761834
 VERSION AZ761834.1 GI:12871174
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunn,D., Ayagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0556 row: E column: 19

Seq primer: CGTTGTAACACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0556E19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 CACCGCGCC 396
 |||||
 Db 10 CACCGCGCC 2

RESULT 41
 AZ782026/c
 LOCUS AZ782026 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0021123R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021123 R, genomic survey sequence.

ACCESSION AZ782026
 VERSION AZ782026.1 GI:12915307
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0021 row: I column: 23

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0021123"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTG 251
 |||||
 Db 11 CACCTCCTG 3

RESULT 42

AZ865832

LOCUS AZ865832

DEFINITION 2M0176D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0176D09 F, genomic survey sequence.

ACCESSION AZ865832

VERSION AZ865832.1 GI:13066534

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Rilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0176 row: D column: 09

Seq primer: CGTTGTAACAGCGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0176D09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 CTACCTGTG 89
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 Db 4 CTACCTGTG 12

RESULT 43
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 DEFINITION
 2M0196J13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0196J13 R, genomic survey sequence.
 ACCESSION
 AZ938271
 VERSION
 AZ938271.1 GI:13797826
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITL
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0196 row: J column: 13

Seq primer: CACACGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="UUGC2M0196J13"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 GGCGCATCC 538
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 Db 9 GGCGCATCC 1

RESULT 44
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 LOCUS
 DEFINITION
 AB088508 lambda Triplex2 rice phloem sap cDNA Oryza sativa (japonica cultivar-group) cDNA clone PA596, mRNA sequence.
 ACCESSION
 AB088508
 VERSION
 AB088508.1 GI:28298607
 KEYWORDS
 EST.
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 1 (bases 1 to 20)
 Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and Fujiwara,T.
 TITL
 Small RNAs detected in the rice phloem sap
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Hironori Mano
 Plant Genome Center Co.,Ltd
 Kannondai-1-25-2, Taikuba, Ibaraki 305-0856, Japan
 Tel: 81-298-39-4823
 Email: hmano@pgcdna.co.jp.
 Location/Qualifiers
 1. .20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="PA596"

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/tissue type="phloem"
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Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 AAAACCATG 466
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Db 5 AAAACCATG 13

RESULT 45
AB094447/c
LOCUS AB094447 20 bp mRNA linear EST 01-MAY-2003
DEFINITION AB094447 lambda Triplex2 rice phloem sap cDNA Oryza sativa
(japonica cultivar-group) cDNA clone PA36, mRNA sequence.
ACCESSION AB094447.1 GI:30307352
VERSION AB094447.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mano,H., Noguchi,M., Oshima,T., Yoneyama,T., Hayashi,H. and
Fujiwara,T.
TITLE Small RNAs detected in the rice phloem sap
JOURNAL Unpublished (2003)
COMMENT Contact: Hironori Mano
Plant Genome Center Co.,Ltd
Kannondall-25-2, Tsukuba, Ibaraki 305-0856, Japan
Tel: 81-298-39-4823
Email: hmano@pcdna.co.jp.

FEATURES
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/db_xref="taxon:39947"
/clone="PA36"
/tissue type="phloem"
/clone_lib="lambda Triplex2 rice phloem sap cDNA"

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Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 TCCTCCGCT 190
|||||
Db 17 TCCTCCGCT 9

RESULT 46
AU060510
LOCUS AU060510 20 bp mRNA linear EST 20-MAY-1999
DEFINITION AU060510 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLK222, mRNA sequence.
ACCESSION AU060510.1 GI:4881614
VERSION AU060510.1
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
TITLE Developmental cDNA in Dictyostelium discoideum
JOURNAL Unpublished (1998)

```

```

COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES
Location/Qualifiers
1..20
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="SLK222"
/dev_stage="slug"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATTCAAAA 49
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Db 4 AATTCAAAA 12

RESULT 47
AU254527/c
LOCUS AU254527 20 bp mRNA linear EST 25-APR-2002
DEFINITION AU254527 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0002395 3', mRNA sequence.
ACCESSION AU254527
VERSION AU254527.1 GI:20316392
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkat@bs.nist-nara.ac.jp, BED/index.html.
URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0002395"
/tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match      1.5%; Score 9; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 TTCAAAAAT 51
|||||
Db 19 TTCAAAAAT 11

RESULT 48
BM395007/c

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LOCUS      BM395007      20 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA (large fraction)
ACCESSION  BM395007
VERSION     BM395007.1  GI:18195060
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
REFERENCE   1 (bases 1 to 20)
AUTHORS     Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
            Frankel, J., and Klobutcher, L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="Tetrahymena thermophila"
               /mol_type="mRNA"
               /strain="CU428.1"
               /db_xref="taxon:5911"
               /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
               /notes="Vector: Bluescript2 SK+; Details on library
               preparation can be found in Chilcoat and Turkewitz (2001)
               Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match      1.5%; Score 9; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      160 GGCTGCCAC 168
Db      17 GGCTGCCAC 9

RESULT 49
LOCUS      CF301771      20 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--06-M03-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
            sativa cDNA clone 7LEAF--06-M03, mRNA sequence.
ACCESSION  CF301771
VERSION     CF301771.1  GI:33673532
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 20)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES    Location/Qualifiers
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               /mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-M03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
ORIGIN
Query Match      1.5%; Score 9; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      454 GTAGAAAAC 462
Db      12 GTAGAAAAC 20

RESULT 50
LOCUS      MUSGS01811  20 bp      mRNA      linear      EST 12-DEC-1995
DEFINITION MUSGS01811 Mouse 3'-directed Mus musculus domesticus cDNA clone
            md1693 3', mRNA sequence.
ACCESSION  D18749
VERSION     D18749.1   GI:1100718
KEYWORDS    EST.
SOURCE      Mus musculus domesticus (western European house mouse)
ORGANISM    Mus musculus domesticus
REFERENCE   1 (bases 1 to 20)
AUTHORS     Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.
TITLE       Analysis of gene expression in mouse embryogenesis by 3'-directed
            cDNA sequencing
JOURNAL     Unpublished (1995)
COMMENT     Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and
            Matsubara, K.
            Institute for Cellular and Molecular Biology
            Osaka University
            3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES    Location/Qualifiers
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               /strain="C57BL/6J"
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               /db_xref="taxon:10092"
               /clone="md1693"
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               /clone_lib="Mouse 3'-directed"
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Query Match      1.5%; Score 9; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43 TTCAAAAAT 51
Db      19 TTCAAAAAT 11

RESULT 51
LOCUS      AZ339898      20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0071N04R Mouse 10kb plasmid UUCGIM library Mus musculus genomic
            clone UUCGIM0071N04 R, genomic survey sequence.
ACCESSION  AZ339898
VERSION     AZ339898.1  GI:10414624
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0071 row: N column: 04
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              Class: Plasmid ends
              High quality sequence stop: 20.
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCLM0071N04"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              Musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [G14732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      427 GATTATTTT 435
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Db      1 GATTATTTT 9

RESULT 52
AZ341907/c
LOCUS      AZ341907      20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION      1M0074F07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0074F07 R, genomic survey sequence.
ACCESSION      AZ341907
VERSION      AZ341907.1 GI:10418624
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)

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```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0074 row: F column: 07
              Seq primer: CACACAGGAACAGCTATGACC
              Class: Plasmid ends
              High quality sequence stop: 20.
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
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                /db_xref="taxon:10090"
                /clone="UUGCLM0074F07"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGCLM library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              Musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [G14732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83 ACCTGTGCT 91
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Db      10 ACCTGTGCT 2

RESULT 53
AZ346729
LOCUS      AZ346729      20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION      1M0082A10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0082A10 F, genomic survey sequence.
ACCESSION      AZ346729
VERSION      AZ346729.1 GI:10425966
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)

```

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
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 /clone="UUGC1M0082A10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 CCAACTCTCA 313
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 Db 9 CCAACTCTCA 17

RESULT 54
 AZ377958/c
 LOCUS AZ377958 20 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0132G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0132G02 R, genomic survey sequence.
 ACCESSION AZ377958
 VERSION AZ377958.1 GI:10491658
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0132 row: G column: 02
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0132G02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
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 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 CTGGAATAC 449
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 Db 12 CTGGAATAC 4

RESULT 55
 AZ429610
 LOCUS AZ429610 20 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0213H12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0213H12 R, genomic survey sequence.
 ACCESSION AZ429610
 VERSION AZ429610.1 GI:10553623
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 20) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
           University of Utah Genome Center
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0213 row: H column: 12
           Seq primer: CACACAGGAACACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 20.
FEATURES      Location/Qualifiers
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               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0213H12"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred.No.1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CCTCTTGAT 17
          |||||
          11 CCTCTTGAT 19

RESULT 56
AZ453505/c
LOCUS      AZ453505
DEFINITION 1M0254M22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0254M22 R, genomic survey sequence.
ACCESSION  AZ453505
VERSION     AZ453505.1 GI:10611371
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 20) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
           University of Utah Genome Center
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0213 row: H column: 12
           Seq primer: CACACAGGAACACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 20.
FEATURES      Location/Qualifiers
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               1..20
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
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               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred.No.1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CCTCTTGAT 17
          |||||
          11 CCTCTTGAT 19

RESULT 57
AZ480596
LOCUS      AZ480596
DEFINITION 1M0302D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0302D18 F, genomic survey sequence.
ACCESSION  AZ480596
VERSION     AZ480596.1 GI:10641661
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0302 row: D column: 18
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0302D18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWP42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTC 183

Db 1 TTGCTCTTC 9

RESULT 58

AZ482160
 LOCUS AZ482160 20 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0307G09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0307G09 F, genomic survey sequence.
 ACCESSION AZ482160
 AZ482160.1 GI:10643225
 GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0307 row: G column: 09
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0307G09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWP42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 GGCTGCACC 391

Db 9 GGCTGCACC 17

RESULT 59

AZ486306/c
 LOCUS AZ486306 20 bp DNA linear GSS 05-OCT-2000
 DEFINITION IM0314B13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0314B13 F, genomic survey sequence.
 ACCESSION AZ486306
 AZ486306.1 GI:10652951
 GSS.
 KEYWORDS Mus musculus (house mouse)
 SOURCE

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0314 row: B column: 13
              Seq primer: GCTTGTAAACGACGCGCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
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                  /db_xref="taxon:10090"
                  /clone="UUGC1M0314B13"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
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                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                  inducible derivative of plasmid R1. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      224  GCTACCGCG 232
Db      18  GCTACCGCG 10
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          |||||

RESULT 60
AZ504441
LOCUS      AZ504441
DEFINITION 1M0344F15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0344F15 R, genomic survey sequence.
ACCESSION  AZ504441
VERSION    AZ504441.1 GI:10685757
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0344 row: F column: 15
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
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                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC1M0344F15"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
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                  electrophoresis. Vector DNA was prepared from a derivative
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                  inducible derivative of plasmid R1. The vector was ligated
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                  purified. The sheared, adaptor mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches      9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      501  AAATTCAGT 509
Db      4   AAATTCAGT 12
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          |||||

RESULT 61
AZ591658
LOCUS      AZ591658
DEFINITION 1M0401F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0401F19 R, genomic survey sequence.
ACCESSION  AZ591658
VERSION    AZ591658.1 GI:11713848
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0401 row: F column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0401F19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 CTGCTGGAA 446
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DB 1 CTGCTGGAA 9

RESULT 62
AZ601483/c
LOCUS
DEFINITION
20 bp DNA linear GSS 13-DEC-2000
1M0419H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0419H15 R, genomic survey sequence.
ACCESSION
AZ601483
VERSION
AZ601483.1 GI:11723673
KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0419 row: H column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0419H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
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electrophoresis. Vector DNA was prepared from a derivative
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adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 ACTGTGCC 274
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DB 12 ACTGTGCC 4

RESULT 63

AZ624669
LOCUS
DEFINITION
20 bp DNA linear GSS 13-DEC-2000
1M0463D01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0463D01 R, genomic survey sequence.
ACCESSION
AZ624669
VERSION
AZ624669.1 GI:11746859
KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (Bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0463 row: D column: 01
 Seq primer: CACACAGGAACAGCTATGACC
 Class: Plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0463D01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnates/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 electrophoresis. Vector DNA was prepared from a derivative
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 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

1. .20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0463D01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
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 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnates/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
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 polynucleotide kinase. Adaptor oligonucleotides were
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 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 TTGTAGAA 459

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Db 7 TTGTAGAA 15

RESULT 64

AZ651194/c

LOCUS

AZ651194 20 bp DNA linear GSS 14-DEC-2000

DEFINITION

IM0521F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0521F18 R, genomic survey sequence.

ACCESSION

AZ651194

VERSION

AZ651194.1 GI:11786441

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (Bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0521 row: F column: 18

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /clone="UUGC1M0521F18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnates/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAAC 309

|||||

Db 11 AACCCCAAC 3

RESULT 65

AZ653361/c

LOCUS

AZ653361 20 bp DNA linear GSS 14-DEC-2000

DEFINITION

IM0527D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0527D04 F, genomic survey sequence.

ACCESSION

AZ653361

VERSION

AZ653361.1 GI:11790507

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0527 row: D column: 04
                Seq primer: CGTTGTAAACGACGCGCCAGT
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0527D04"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 CAAAAATGT 53
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Db 20 CAAAAATGT 12

RESULT 66
LOCUS      AZ655977/c
DEFINITION 1M0531E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0531E13 F, genomic survey sequence.
ACCESSION  AZ655977
VERSION     AZ655977.1 GI:11793123
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

```

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0531 row: E column: 13
                Seq primer: CGTTGTAAACGACGCGCCAGT
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                High quality sequence stop: 20.
                Location/Qualifiers
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                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
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                was blunt end-repaired with T4 DNA polymerase and T4
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                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
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                with adaptors complementary to the insert adaptors and
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                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."

ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GAGGGAACC 304
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Db 9 GAGGGAACC 1

RESULT 67
LOCUS      AZ656648
DEFINITION 1M0532P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0532P16 F, genomic survey sequence.
ACCESSION  AZ656648
VERSION     AZ656648.1 GI:11793794
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0532 row: P column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 GGAAGGGGCT 494
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Db 5 GGAAGGGCT 13

RESULT 68
AZ776071

LOCUS AZ776071 20 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0009L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0009L24 F, genomic survey sequence.

ACCESSION AZ776071

VERSION AZ776071.1 GI:12903267

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: L column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
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/clone="UUGC2M0009L24"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 GAAGGGGCTG 495
|||||
Db 11 GAAGGGGCTG 19

RESULT 69
AZ780925

LOCUS AZ780925 20 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0018A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0018A16 R, genomic survey sequence.

ACCESSION AZ780925

VERSION AZ780925.1 GI:12913099

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

```

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0018 row: A column: 16
                Seq primer: CACACAGGAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers
FEATURES       1..20
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0018A16"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CAGTCTGAG 320
    |||||
DB 8 CAGTCTGAG 16

RESULT 70
AZ820009
LOCUS
DEFINITION      2M0091P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0091P23 R, genomic survey sequence.
ACCESSION      AZ820009
VERSION        AZ820009.1 GI:12989917
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0018 row: A column: 16
                Seq primer: CACACAGGAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers
FEATURES       1..20
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0018A16"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CAGTCTGAG 320
    |||||
DB 8 CAGTCTGAG 16

RESULT 70
AZ820009
LOCUS
DEFINITION      2M0091P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0091P23 R, genomic survey sequence.
ACCESSION      AZ820009
VERSION        AZ820009.1 GI:12989917
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0091 row: P column: 23
                Seq primer: CACACAGGAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers
FEATURES       1..20
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                /clone="UUGC2M0091P23"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      1.5%; Score 9; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TGCAATAG 409
    |||||
DB 11 TGCAATAG 19

RESULT 71
AZ822878
LOCUS
DEFINITION      2M0096E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0096E02 R, genomic survey sequence.
ACCESSION      AZ822878
VERSION        AZ822878.1 GI:12992786
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

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ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0096 row: E column: 02
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0096202"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
source

1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0096202"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 CCGCGCGCG 398

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 6 CCGCGCGCG 14

Db

RESULT 72

AZ833695/c

LOCUS

DEFINITION

AZ833695

ACCESSION

VERSION

KEYWORDS

SOURCE

AZ833695 20 bp DNA linear GSS 20-FEB-2001
 2M0115N20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGC2M0115N20 R, genomic survey sequence.

Accession AZ833695.1 GI:13003603
 Version AZ833695.1
 Keywords GSS.
 Source Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0115 row: N column: 20
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="UUGC2M0115N20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
source

1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0115N20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (G1[4732114|gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 1.5%; Score 9; DB 28; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCG 380

|||||||
 10 GGGGCTGCG 2

Db

RESULT 73

TA207B03Q

LOCUS

DEFINITION

TA207B03Q

ACCESSION

VERSION

KEYWORDS

SOURCE

TA207B03Q 20 bp DNA linear GSS 13-DEC-2000
 T. brucei sheared genomic DNA clone 207b03, reverse sequence,
 genomic survey sequence.

Accession TA207B03Q.1 GI:11842591
 Version AL475823
 Keywords GSS.
 Source Trypanosoma brucei


```

ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
Location/Qualifiers
1..20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="207b03"
ORIGIN
Query Match 1.5%; Score 9; DB 29; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 492 GCTGCATGA 500
Db 8 GCTGCATGA 16
RESULT 74
CF313731/c
LOCUS
DEFINITION
CF313731 8 bp mRNA linear EST 15-AUG-2003
HD--01-P12.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
ACCESSION
CF313731
VERSION
CF313731.1 GI:33685492
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 8)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongju University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..8
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-P12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOP0; Site_1: EcoRI; Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.7e+09;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 458 AARACCAT 465
Db 8 AARACCAT 1
RESULT 75
BG925375
LOCUS
DEFINITION
BG925375 10 bp mRNA linear EST 06-NOV-2001
HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG925375
VERSION
BG925375.1 GI:14319898
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL
Osteoarthritis Cartilage cDNA libraries
MEDLINE
21482651
PUBMED
11597177
COMMENT
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="HNC (Human Normal Cartilage)"
/notes="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 532 CGCATCCT 539
Db 3 CGCATCCT 10

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RESULT 76
BQ585171
LOCUS
DEFINITION
  S014222-024-001-J02-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
  cDNA clone 024-001-J02-5-PRIME, mRNA sequence.
ACCESSION
  BQ585171
VERSION
  BQ585171.1 GI:26114753
SOURCE
  EST.
  Beta vulgaris
  Beta vulgaris
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 11)
  Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  MEDLINE
  PUBMED
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 11 Std Error: 0.00
  Plate: 1 row: J column: 02
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES
  source
    1..11
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    /mol_type="mRNA"
    /cultivar="KWS320 (double haploid, monogerm breeding
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    /db_xref="taxon:161934"
    /clone="024-001-J02"
    /tissue_type="inflorescence"
    /lab_host="EMDH108"
    /notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet, library provided by KWS
    Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
  Query Match 1.3%; Score 8; DB 13; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 457 GAAACCA 464
  Db 1 GAAACCA 8
  |||||
  RESULT 77
  CF300559/c
  LOCUS
  DEFINITION
    7LEAF--05-B09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
    sativa cDNA clone 7LEAF--05-B09, mRNA sequence.
  ACCESSION
    CF300559
  VERSION
    CF300559.1 GI:33672320
  KEYWORDS
    EST.
  SOURCE
    Oryza sativa
    Oryza sativa
  1..11
  Location/Qualifiers
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--05-B09"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 11;
  Best Local Similarity 100.0%; Pred. No. 4.3e-07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 429 TTATTTT 436
  Db 9 TTATTTT 2
  |||||
  RESULT 78
  BH213431/c
  LOCUS
  DEFINITION
    BH213431 Arabidopsis thaliana TDNA insertion lines Arabidopsis
    thaliana genomic clone SALK_009214, genomic survey sequence.
  ACCESSION
    BH213431
  VERSION
    BH213431.1 GI:16395344
  KEYWORDS
    GSS.
  SOURCE
    Arabidopsis thaliana (thale cress)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
  REFERENCE
    1 (bases 1 to 11)
    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
    Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
    Shinn,P., Zimmerman,J. and Ecker,J.R.
    A Sequence-Indexed Library of Insertion Mutations in the
    Arabidopsis Genome
    Unpublished (2001)
  JOURNAL
    COMMENT
    Contact: Joseph R. Ecker
    Salk Institute Genomic Analysis Laboratory (SIGnAL)
    The Salk Institute for Biological Studies
    10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
    Tel: 858 453 4100 x1752
    Fax: 858 558 6379
    Email: ecker@salk.edu
    This is single pass sequence recovered from the left border of
    TDNA.
  CLASS: TDNA tagged.
  FEATURES
    source
      1..11
      Location/Qualifiers

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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GALK 009214"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497
Db 11 GGGCTGCA 4

RESULT 79
BG925521/c
LOCUS
DEFINITION HNC5-1-D3_R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG925521
VERSION BG925521.1 GI:14320044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
source 1..12
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

FEATURES
Query Match 1.3%; Score 8; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGAGGG 492
Db 8 GGGAGGG 1

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GALK 009214"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497
Db 11 GGGCTGCA 4

RESULT 79
BG925521/c
LOCUS
DEFINITION HNC5-1-D3_R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG925521
VERSION BG925521.1 GI:14320044
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
source 1..12
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

FEATURES
Query Match 1.3%; Score 8; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGAGGG 492
Db 8 GGGAGGG 1

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RESULT 80
CF280439
LOCUS
DEFINITION 14ETL--07-B21.bi Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-B21, mRNA sequence.
ACCESSION CF280439
VERSION CF280439.1 GI:33657825
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
source 1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--07-B21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 CCTTCAA 426
Db 3 CCTTCAA 10

CF311969
LOCUS
DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-H13, mRNA sequence.
ACCESSION CF311969
VERSION CF311969.1 GI:33683730
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF-07-H13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CGTGACAG 113

Db 9 CGTGACAG 2

RESULT 82

CF329021/c

LOCUS 12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-D03.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-D03, mRNA sequence.

ACCESSION CF329021

VERSION CF329021.1 GI:33806279

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. .12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTT 435

Db 10 ATTATTTT 3

RESULT 83

BG927437

LOCUS 13 bp mRNA linear EST 06-NOV-2001
DEFINITION HNC1-1-H7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG927437

VERSION BG927437.1 GI:14321960

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 13)

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Satche, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL 21482651

MEDLINE 11597177

PUBMED

COMMENT

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7.

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI; Directional"

ORIGIN

Query Match 1.3%; Score 8; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 CTTTCGTC 295

Db 3 CTTTCGTC 10

RESULT 84

BQ582420

LOCUS 13 bp mRNA linear EST 06-DEC-2002
DEFINITION BQ582420-024-001-J02-SP6 MP12-ADIS-024-Inflorcescence Beta vulgaris cDNA clone 024-001-J02 5-PRIME, mRNA sequence.

ACCESSION BQ582420

VERSION BQ582420.1 GI:26111997

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

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REFERENCE
AUTHORS      1 (bases 1 to 13)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 13 Std Error: 0.00
              Plate: 1 row: J column: 02
              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES     source
              1..13
              Location/Qualifiers
                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="GABI:181155"
                /db_xref="taxon:161934"
                /clone="024-001-J02"
                /tissue_type="inflorescence"
                /lab_host="EMDH10B"
                /clone_lib="MPIZ-ADIS-024-inflorescence"
                /note="Vector: pCMVSPORT6; Site 1: Sali; site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulzek@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      457 GAAACCA 464
        |||||
        1 GAAACCA 8

RESULT 85
BQ595423/c
LOCUS      BQ595423
DEFINITION      13 bp mRNA linear EST 06-DEC-2002
                cDNA clone 024-022-N20 5-PRIME, mRNA sequence.
ACCESSION      BQ595423
VERSION        BQ595423.1 GI:26125006
KEYWORDS       EST.
SOURCE         Beta vulgaris
ORGANISM       Beta vulgaris
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698

REFERENCE
AUTHORS      1 (bases 1 to 13)
              Weisshaar B
              ADIS DNA core facility at MPiZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 13 Std Error: 0.00
              Plate: 22 row: N column: 20
              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES     source
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                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="GABI:191428"
                /db_xref="taxon:161934"
                /clone="024-022-N20"
                /tissue_type="developing root"
                /lab_host="EMDH10B"
                /clone_lib="MPIZ-ADIS-024-developing root"
                /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulzek@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 GTGGAATT 176
        |||||
        11 GTGGAATT 4

RESULT 86
CF291168/c
LOCUS      CF291168
DEFINITION      13 bp mRNA linear EST 14-AUG-2003
                14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
                sativa cDNA clone 14ROOT--01-H20, mRNA sequence.
ACCESSION      CF291168
VERSION        CF291168.1 GI:33660201
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
TITLE          Contact: Nahm B.H.
JOURNAL        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Gyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnaahm@gbio.com, bnaahm@bio.myongji.ac.kr.
FEATURES     source
              1..13
              Location/Qualifiers
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"

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/clone="14ROOT--01-H20"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
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 Db 8 TTATTTT 1

RESULT 87

CF306647 13 bp mRNA linear EST 15-AUG-2003
 LOCUS HDAL--04-H13.g1 OshDAC1-overexpressing transgenic rice lambda phage
 DEFINITION cDNA library 1 (HDAL) Oryza sativa cDNA clone HDAL--04-H13, mRNA
 sequence.

ACCESSION CF306647.1 GI:33678408
 VERSION CF306647
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 13)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
 1..13
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HDAL--04-H13"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOLR"
 /clone_lib="OshDAC1-overexpressing transgenic rice lambda
 phage cDNA library 1 (HDAL)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Callus was treated with ABA (20um) for 1hour. cDNA
 was inserted into lambda Uni-ZAP XR vector at 5' end with
 EcoRI and 3' end with XhoI site. mRNA was derived from
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 489 AGGCGTCG 496
 |||||
 Db 6 AGGCGTCG 13

RESULT 88

CF921303/c 13 bp mRNA linear EST 05-NOV-2003
 LOCUS gmrHrw3-07 GI2.1.084 Soybean root hair subtracted cDNA library
 DEFINITION gmrHrw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF921303
 VERSION CF921303.1 GI:38192097
 KEYWORDS EST.

SOURCE

ORGANISM Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE

1 (bases 1 to 13)
 Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
 Expressed sequence tags from soybean root hair subtractive cDNA
 library

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)
 Contact: Gary Stacey
 University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752
 Fax: 573-882-0588
 Email: stacey@missouri.edu
 Single pass sequence
 Seq primer: T7.

FEATURES

source
 1..13
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /tissue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library
 gmrHrw3"
 /notes="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 TCCTTTTC 128
 |||||
 Db 13 TCCTTTTC 6

RESULT 89

BM397622 14 bp mRNA linear EST 17-JAN-2002
 LOCUS 5009-0-35-C02.t.2 Chilcoat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM397622
 VERSION BM397622.1 GI:18197675
 KEYWORDS EST.

SOURCE

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE

1 (bases 1 to 14)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.

AUTHORS

TITLE

JOURNAL

COMMENT

EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source Location/Qualifiers

1..14
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 1.3%; Score 8; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368
|||||
Db 5 GCTGAGCC 12

RESULT 90

BQ589337/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

14 bp mRNA linear EST 06-DEC-2002

S014007-024-015-002-SP6 MP12-ADIS-024-storage root Beta vulgaris

cDNA clone 024-015-002 5-PRIME, mRNA sequence.

BQ589337

QY589337.1

GI:26118920

EST.

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert length: 14 Std Error: 0.00

Plate: 15 row: 0 column: 02

Seq primer: SP6; CATACGATTAGTGACACTATAG.

1..14

Location/Qualifiers

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:187733"

/db_xref="taxon:161934"

/clone="024-015-002"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP12-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTTCITT 37
|||||
Db 9 GTTTCITT 2

RESULT 91

CA853334/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

14 bp mRNA linear EST 01-AUG-2003

B07A06 seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone

B07A06 5', mRNA sequence.

CA853334

CA853334.1

GI:33390127

EST.

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 14)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean

infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ars.usda.gov.

1..14

Location/Qualifiers

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B07A06"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA

extracted from roots of soybean cv. Peking 12 hrs after

infection by SCN race 3. These are cloned in pBluescript

SK- phagemid."

1..14

Location/Qualifiers

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B07A06"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA

extracted from roots of soybean cv. Peking 12 hrs after

infection by SCN race 3. These are cloned in pBluescript

SK- phagemid."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTT 182
|||||
Db 11 TTGCTCTT 4

RESULT 92

CF301021/c

LOCUS

DEFINITION

ACCESSION

VERSION

14 bp mRNA linear EST 15-AUG-2003

7LEAF--05-L10.gi Rice leaf plasmid cDNA library 11 (7LEAF) Oryza

sativa cDNA clone 7LEAF--05-L10, mRNA sequence.

CF301021

CF301021.1

GI:33672782

```

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..14
location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-L10"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR-to-PO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
|||||
Db 9 TTATTTT 2

RESULT 93
BF219911
LOCUS 601296879T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961653 3',
EST. mRNA sequence.
ACCESSION BF219911.1 GI:11126005
VERSION BF219911
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRALI row: n column: 20
High quality sequence stop: 5.

FEATURES
source
1..15
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:2961653"
/tissue_type="thabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```



```

CDNA clone 024-023-U24 5-PRIME, mRNA sequence.
ACCESSION   BQ594980
VERSION     BQ594980.1  GI:26124563
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 23 row: J column: 24
Seq primer: SP6; CATACGATTWAGGTGACACTATAG.
FEATURES    Location/Qualifiers
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               /mol_type="mRNA"
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               line)"
               /db_xref="GABI:191878"
               /db_xref="taxon:161934"
               /clone="024-023-J24"
               /tissue_type="developing root"
               /lab_host="EMDH108"
               /clone_lib="MPZ-ADIS-024-developing root"
               /note="Vector: pCMVSPORT6; site 1: SalI; Site 2: NotI;
               cDNA library from sugar beet, library provided by KWS
               Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
               b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-r7; Note:
               Sequencing granted in the context of the GABI-Beet
               project, local PI: Dr. Katharina Schneider, coordinator:
               Prof. Christian Jung; Sequence submission managed by
               RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
Db 6 TTTTACT 13

RESULT 96
CA796369
LOCUS       CA796369
DEFINITION  Cac BL_3383 Cac BL (Bean and Leaf from Amelonado type Cacao)
Theobroma cacao cDNA clone Cac_BL_3383 5', mRNA sequence.
ACCESSION   CA796369
VERSION     CA796369.1  GI:26053445
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
ORGANISM    Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;

CDNA clone 024-023-U24 5-PRIME, mRNA sequence.
ACCESSION   BQ594980
VERSION     BQ594980.1  GI:26124563
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 23 row: J column: 24
Seq primer: SP6; CATACGATTWAGGTGACACTATAG.
FEATURES    Location/Qualifiers
             source
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               /organism="Beta vulgaris"
               /mol_type="mRNA"
               /cultivar="KWS2320 (double haploid, monogerm breeding
               line)"
               /db_xref="GABI:191878"
               /db_xref="taxon:161934"
               /clone="024-023-J24"
               /tissue_type="developing root"
               /lab_host="EMDH108"
               /clone_lib="MPZ-ADIS-024-developing root"
               /note="Vector: pCMVSPORT6; site 1: SalI; Site 2: NotI;
               cDNA library from sugar beet, library provided by KWS
               Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
               b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-r7; Note:
               Sequencing granted in the context of the GABI-Beet
               project, local PI: Dr. Katharina Schneider, coordinator:
               Prof. Christian Jung; Sequence submission managed by
               RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      1.3%; Score 8; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
Db 6 TTTTACT 13

RESULT 96
CA796369
LOCUS       CA796369
DEFINITION  Cac BL_3383 Cac BL (Bean and Leaf from Amelonado type Cacao)
Theobroma cacao cDNA clone Cac_BL_3383 5', mRNA sequence.
ACCESSION   CA796369
VERSION     CA796369.1  GI:26053445
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
ORGANISM    Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;

Theobroma.
1 (bases 1 to 15)
Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
MEDLINE     22337596
PUBMED      12447539
COMMENT     Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES    Location/Qualifiers
             source
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               /organism="Theobroma cacao"
               /mol_type="mRNA"
               /strain="Amelonado type"
               /db_xref="taxon:3641"
               /clone="Cac BL_3383"
               /tissue_type="Mature leaf and mature bean"
               /cell_type="Whole organ"
               /dev_stage="maturity"
               /lab_host="XL-1 Blue MRF"
               /clone_lib="Cac BL (Bean and Leaf from Amelonado type
               Cacao)"
               /note="Vector: pBK-CMV; Bean and leaf tissue from an
               Amelonado type Cacao tree."
ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 348 TGAGGACC 355
Db 3 TGAGGACC 10

RESULT 97
CF290849/c
LOCUS       CF290849
DEFINITION  14ROOT--01-A17-g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION   CF290849
VERSION     CF290849.1  GI:33659882
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="Oryza sativa"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:4530"
               /clone="14ROOT--01-A17"

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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436
Db 8 TTATTTT 1

RESULT 98
CF291030/c      15 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-E19"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436
Db 10 TTATTTT 3

RESULT 99
CF291030/c      15 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--06-F02-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--06-F02, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-F02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN

Query Match      1.3%; Score 8; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 100
AA881100
LOCUS
DEFINITION
v206d08.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1314927 5' Similar to SW:UBCI_HUMAN P50550
UBIQUITIN-CONJUGATING ENZYME E2-18 KD ; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 16)
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

```

Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:685223

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

source

1. .16
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314927"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACCATCTGAAGTGGAGCGCGCCGCGAATGTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaudo."

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCCTCC 187
|||||
Db 10 CTTCCTCC 3

RESULT 102

AA937877

LOCUS

DEFINITION

AA937877 16 bp mRNA linear EST 30-APR-1998
nw90e06.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1253890
similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ; mRNA
sequence.

AA937877 1 GI:3095988

VERSION AA937877.1

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,

Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

1. .16
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314927"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCACCATCTGAAGTGGAGCGCGCCGCGAATGTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaudo."

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30

|||||

Db 3 GGAGGAAG 10

RESULT 101

AA881100/c

LOCUS

DEFINITION

AA881100 16 bp mRNA linear EST 26-MAR-1998
vz06d08.r1 Soares mammary_gland NbMMG Mus musculus cDNA clone
IMAGE:1314927 5' similar to SW:UBCI HUMAN P50550
UBIQUITIN-CONJUGATING ENZYME E2-18 KD ; mRNA sequence.

AA881100 1 GI:2990410

VERSION AA881100.1

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 16)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterson, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

```

source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1253890"
/sex="male"
/tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr12"
/note="Vector: PAMP10; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dt priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN
Query Match 1.3%; Score 8; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
|||||
9 TTATTTT 16

RESULT 103
BG926060
LOCUS
DEFINITION HNC23-1-E1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG926060
VERSION BG926060.1 GI:14320583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 16)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar1@gsk.com
Seq primer: T7.

FEATURES
source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCCT 185
|||||

source
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCCT 185
|||||

```

```

Db 5 CTCCTCCT 12

RESULT 104
CF920788/c
LOCUS
DEFINITION smrRw3-01_E05_1_039 Soybean root hair subtracted cDNA library
smrRw3 Glycine max cDNA, mRNA sequence.
ACCESSION CF920788
VERSION CF920788.1 GI:38191582
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 16)
AUTHORS Schaffer,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
TITLE Expressed sequence tags from soybean root hair subtractive cDNA
library
JOURNAL Unpublished (2003)
COMMENT Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: stacey@missouri.edu
Single pass sequence
Seq primer: T7.

FEATURES
source
1. .16
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
smrRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30
|||||
11 GGAGGAAG 4

RESULT 105
AW247673
LOCUS
DEFINITION AW247673
ACCESSION AW247673
VERSION AW247673.1 GI:6590666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2820207.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

AW247673 17 bp mRNA linear EST 07-JAN-2000
2820207.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820207 5',
mRNA sequence.
AW247673
AW247673.1 GI:6590666
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2820207.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

```

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.

Plate: L1CM3 row: J column: 16.

FEATURES

Location/Qualifiers
1. 17

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820207"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 GCCCGAGG 373
|||||||
Db 2 GCCCGAGG 9

RESULT 106

AW247949
LOCUS
DEFINITION
AW247949 17 bp mRNA linear EST 07-JAN-2000
2820605.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820605 3', mRNA sequence.

ACCESSION

AW247949
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820605.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

REFERENCE

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous

COMMENT

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM6 row: L column: 8
High quality sequence stop: 17.

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM4 row: K column: 6.

FEATURES

Location/Qualifiers
1. 17

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820605"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
|||||||
Db 6 TTTTACT 13

RESULT 107

AW251033/c
LOCUS
DEFINITION
AW251033 17 bp mRNA linear EST 07-JAN-2000
2821399.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821399 3', mRNA sequence.

ACCESSION

AW251033
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821399.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

REFERENCE

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM6 row: L column: 8
High quality sequence stop: 17.

COMMENT

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1CM6 row: L column: 8
High quality sequence stop: 17.

FEATURES

Location/Qualifiers

1..17
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821399"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.7e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 TCAAAA 50
 |||||
 Db 13 TCAAAA 6

RESULT 108

BM399748

LOCUS

5009-0-60-H02.t.1

DEFINITION

Tetrahymena thermophila cDNA (large fraction)

ACCESSION

BM399748

VERSION

EST.

KEYWORDS

Tetrahymena thermophila

SOURCE

Tetrahymena thermophila

ORGANISM

Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 17)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J., and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..17

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 1.3%; Score 8; DB 12; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.7e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 326 TCACCGCG 333

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Db 8 TCACCGCG 15

RESULT 109

BQ591588

LOCUS

E012616-024-017-C15-SP6

DEFINITION

cDNA clone 024-017-C15 5-PRIME, mRNA sequence.

ACCESSION

BQ591588

VERSION

EST.

KEYWORDS

Beta vulgaris

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.

and Radloff, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert length: 17 Std Error: 0.00

Plate: 17 row: C column: 15

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source

1..17

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="XWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:188532"

/db_xref="taxon:161934"

/clone="024-017-C15"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.7e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 429 TTATTTT 436

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Db 1 TTATTTT 8

RESULT 110

CA797283

LOCUS

CA797283

DEFINITION

Cac_BL_4376 Cac.BL (Bean and Leaf from Amelonardo type Cacao)

Theobroma cacao cDNA clone Cac_BL_4376 5', mRNA sequence.

CA797283

ACCESSION

CA797283

VERSION

CA797283.1 GI:26054369

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KEYWORDS
SOURCE      Theobroma cacao (cacao)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
TITLE      Gene discovery and microarray analysis of cacao (Theobroma cacao
            L.) varieties
JOURNAL    Planta 216 (2), 255-264 (2002)
MEDLINE    22337596
PUBMED     12447539
COMMENT    Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644
            Email: Paul.Jones@eu.affem.com
            Seq primer: T3.
FEATURES   Location/Qualifiers
            source
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            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
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            /clone="Cac BL 4376"
            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"
            /lab_host="XL-1 Blue MRF"
            /clone_lib="Cac_BL (Bean and Leaf from Amelonado type
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            /note="Vector: pBK-CMV; Bean and leaf tissue from an
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Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      237 CTGGTTCA 244      17 bp mRNA linear EST 05-DEC-2002
      |||||
      10 CTGGTTCA 17      CAC BL 4642 Cac BL (Bean and Leaf from Amelonado type Cacao)
      Theobroma cacao_cDNA clone Cac_BL_4642 5', mRNA sequence.

RESULT 111
CA797566/1 17 bp mRNA linear EST 05-DEC-2002
LOCUS      CAC BL 4642 Cac BL (Bean and Leaf from Amelonado type Cacao)
DEFINITION Theobroma cacao_cDNA clone Cac_BL_4642 5', mRNA sequence.
ACCESSION  CA797566.1 GI:26054652
VERSION     CA797566.1
KEYWORDS    EST.
SOURCE      Theobroma cacao (cacao)
ORGANISM    Theobroma cacao
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
TITLE      Gene discovery and microarray analysis of cacao (Theobroma cacao
            L.) varieties
JOURNAL    Planta 216 (2), 255-264 (2002)
MEDLINE    22337596
PUBMED     12447539
COMMENT    Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644

KEYWORDS
SOURCE      Theobroma cacao (cacao)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
TITLE      Gene discovery and microarray analysis of cacao (Theobroma cacao
            L.) varieties
JOURNAL    Planta 216 (2), 255-264 (2002)
MEDLINE    22337596
PUBMED     12447539
COMMENT    Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644

Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES   Location/Qualifiers
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            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
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            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"
            /lab_host="XL-1 Blue MRF"
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            /note="Vector: pBK-CMV; Bean and leaf tissue from an
            Amelonado type Cacao tree."
ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      409 GCCATCAT 416      17 bp mRNA linear EST 15-AUG-2003
      |||||
      13 GCCATCAT 6      7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
      sativa cDNA clone 7LEAF--03-N22, mRNA sequence.

RESULT 112
CF299737/1 17 bp mRNA linear EST 15-AUG-2003
LOCUS      7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-N22, mRNA sequence.
ACCESSION  CF299737.1 GI:33671498
VERSION     CF299737.1
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzoae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="7LEAF--03-N22"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E. coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      46 AAAATGT 53
Db      15 AAAATGT 8

RESULT 113
CF310268
LOCUS   ABF--04-N06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION
ACCESSION CF310268
VERSION   CF310268
KEYWORDS  Oryza sativa cDNA clone ABF--04-N06, mRNA sequence.
SOURCE    EST.
ORGANISM  Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
          Location/Qualifiers
            1..17
              /organism="Oryza sativa"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:4530"
              /clone="ABF--04-N06"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="ABF3-overexpressing transgenic rice plasmid
              cDNA library (ABF)"
              /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
              for 2hrs. Oligo-capped mRNA was reverse transcribed and
              then used for PCR. mRNA was prepared from ABA-responsive
              element binding transcription factor 3 overexpression
              line."
ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      129 ACTGGACT 136
Db      8 ACTGGACT 15

PCH303755
LOCUS   Plasmodium chabaudi genome survey sequence, clone PC7C5.plt,
DEFINITION
ACCESSION AJ303755
VERSION   AJ303755.1 GI:11140262
KEYWORDS  GSS: genome survey sequence.
SOURCE    Plasmodium chabaudi
ORGANISM  Plasmodium chabaudi
          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
          Bowman,S., Phillips,R.S. and Turner,C.M.
          Gene discovery in Plasmodium chabaudi by genome survey sequencing

JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE 21192558
PUBMED 11295179
REFERENCE 2 (bases 1 to 17)
AUTHORS Janssen,C.S.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2000) Division of Infection & Immunity,
COMMENT University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
          bases 39 to 55 (QL to SR).
FEATURES Location/Qualifiers
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            /organism="Plasmodium chabaudi"
            /mol_type="genomic DNA"
            /db_xref="taxon:5825"
            /clone="PC7C5.plt"

ORIGIN
Query Match 1.3%; Score 8; DB 29; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      430 TATTTTAA 437
Db      6 TATTTTAA 13

RESULT 115
AW246505
LOCUS   2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
DEFINITION mRNA sequence.
ACCESSION AW246505
VERSION   AW246505.1 GI:65899498
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Other ESTs: 2821585.5prime
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs@mail.nih.gov
          Tissue Procurement: DCTD/DP cDNA Library Preparation: Ling
          Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
          Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
          project
          Project Clone distribution: MGC clone distribution information can
          be found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu/Low Quality Sequence: 18
          contiguous PHRED high quality bases following vector sequence. Very
          Low Quality Sequence: trace file contained 18 contiguous distinct
          peaks following vector sequence. Polyadenylation: Based upon the
          presence of a XhoI site followed by a run of 14 or more T residues
          at the beginning of the sequence, this cDNA insert was
          polyadenylated.
          Plate: L1CM7 row: D column: 2
          High quality sequence stop: 18.
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              /tissue_type="small cell carcinoma"
              /cell_line="MGC3"
              /lab_host="DH10B (phage-resistant)"

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/clone lib="NIH_MGC 7"
/Note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match
Best Local Similarity 1.3%; Score 8; DB 10; Length 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 TTTCTTTA 38
Db 8 TTTCTTTA 15
RESULT 116
BG927414
LOCUS
DEFINITION
HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG927414.1 GI:14321937
VERSION
BG927414.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE
21482651
PUBMED
11597177
COMMENT
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
FEATURES
Location/Qualifiers
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1..18
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/db_xref="taxon:9606"
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/Note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
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Query Match
Best Local Similarity 1.3%; Score 8; DB 12; Length 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 513 TCTCTCCA 520
Db 9 TCTCTCCA 16
RESULT 117
BM395336
LOCUS
DEFINITION
50072-2-8-F05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395336
VERSION
BM395336.1 GI:18195389
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
source
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/Note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
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Best Local Similarity 1.3%; Score 8; DB 12; Length 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 GGACTGGG 205
Db 1 GGACTGGG 8
RESULT 118
BM395686
LOCUS
DEFINITION
5009-0-10-B05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395686
VERSION
BM395686.1 GI:18195739
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
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1..18
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/mol_type="mRNA"

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Query Match 1.3%; Score 8; DB 12; Length 18;
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Qy 326 TCACCGCG 333
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 Db 5 TCACCGCG 12

RESULT 122
 BQ584794/c
 LOCUS
 DEFINITION BQ584794 18 bp mRNA linear EST 06-DEC-2002
 E011573-024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris
 cDNA clone 024-002-E13 5-PRIME, mRNA sequence.

ACCESSION BQ584794
 VERSION BQ584794.1 GI:26114371
 KEYWORDS EST.

SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 18)
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE
 PUBMED 22362189

COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 Plate: 2 row: E column: 13
 Seq primer: SP6r; ATTAGTGACACTATAGAGA.

FEATURES
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 /cultivar="KWS2320 (double haploid, monogerm breeding
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 /db_xref="GABI:181907"
 /db_xref="taxon:161934"
 /clone="024-002-E13"
 /tissue_type="inflorescence"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-inflorescence"
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Binbeck, Germany, contact:
 b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
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Qy 301 AACCCCAA 308
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 Db 17 AACCCCAA 10

RESULT 123
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 024-013-B09 5-PRIME, mRNA sequence.

ACCESSION BQ586069
 VERSION BQ586069.1 GI:26115651
 KEYWORDS EST.

SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 18)
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE
 PUBMED 22362189

COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 Seq primer: SP6; CATACGATTAGTGACACTATAG.

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 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Binbeck, Germany, contact:
 b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 4.8e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CAAAAATG 52
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 Db 8 CAAAAATG 15

RESULT 124
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 LOCUS
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 E012616-024-017-G11-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-017-G11 5-PRIME, mRNA sequence.

ACCESSION BQ591606
 VERSION BQ591606.1 GI:26121189
 KEYWORDS EST.

SOURCE Beta vulgaris

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ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS      Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.
and Radolof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Email: weishaar@piz-koeln.mpg.de
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 TTTTCACT 131
Db 4 TTTTCACT 11

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LOCUS      HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
DEFINITION
sequence.
ACCESSION  C00629
VERSION    C00629.1 GI:1432859
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 18)
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see , http://www.imcb.osaka-u.ac.jp/bodymap'. The
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 GATCTTCA 328
Db 4 GATCTTCA 328

RESULT 126
C00629
LOCUS      HUMGS0005154 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION  C21365
VERSION    C21365.1 GI:1622475
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 18)
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see , http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 457 GAAAAACCA 464
Db 10 GAAAAACCA 17

RESULT 126
C21365
LOCUS      HUMGS0005154 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION  C21365
VERSION    C21365.1 GI:1622475
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 18)
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see , http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 457 GAAAAACCA 464
Db 10 GAAAAACCA 17

```

```

Osaka University
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
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sequences of the clones represented by this GS sequences is also
found there.
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 457 GAAAAACCA 464
Db 10 GAAAAACCA 17

RESULT 126
C21365
LOCUS      HUMGS0005154 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION  C21365
VERSION    C21365.1 GI:1622475
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 18)
BodyMap; human gene expression database
Unpublished (1995)
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see , http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.
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/notes="One or more human adult tissue"
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 GATCTTCA 328
Db 4 GATCTTCA 328

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Db      1  GATCTTCA 8

RESULT 127
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LOCUS   18 bp mRNA linear EST 01-AUG-2003
DEFINITION
CDNA clone D15F01 5', mRNA sequence.
ACCESSION
CA851607
VERSION 1
KEYWORDS
SOURCE  GI:33388400
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 18)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

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extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 100.0%; Pred.No.4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 GCTACATC 122
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Db 4 GCTACATC 11

RESULT 128
CF308804
LOCUS   18 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--02-M04.G1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-M04, mRNA sequence.
ACCESSION
CF308804
VERSION 1
KEYWORDS
SOURCE  GI:33680565
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Db      1  GATCTTCA 8

RESULT 127
CA851607
LOCUS   18 bp mRNA linear EST 01-AUG-2003
DEFINITION
CDNA clone D15F01 5', mRNA sequence.
ACCESSION
CA851607
VERSION 1
KEYWORDS
SOURCE  GI:33388400
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 18)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
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Location/Qualifiers
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extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 100.0%; Pred.No.4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 GCTACATC 122
|||||
Db 4 GCTACATC 11

RESULT 128
CF308804
LOCUS   18 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--02-M04.G1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-M04, mRNA sequence.
ACCESSION
CF308804
VERSION 1
KEYWORDS
SOURCE  GI:33680565
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred.No.4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96
|||||
Db 2 GCTACGTA 9

RESULT 129
CF309376
LOCUS   18 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.
ACCESSION
CF309376
VERSION 1
KEYWORDS
SOURCE  GI:33681137
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive

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element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 432 TTTTACT 439
Db 11 TTTTACT 18

RESULT 130
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DEFINITION ABF--05-G10-g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-G10, mRNA sequence.
ACCESSION CF310639
VERSION CF310639.1 GI:33682400
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 131
LOCUS CF314452 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-P15-g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--02-P15, mRNA sequence.
ACCESSION CF314452
VERSION CF314452.1 GI:33686213
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
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/cdna_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 132
LOCUS CF314887 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--03-J15-g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION CF314887
VERSION CF314887.1 GI:33686648
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 133
LOCUS CF314887 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--03-J15-g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION CF314887
VERSION CF314887.1 GI:33686648
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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COMMENT Contact: Nahm B.H.
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

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KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 132
LOCUS CF314887 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--03-J15-g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION CF314887
VERSION CF314887.1 GI:33686648
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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cDNA library (HD)"
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

RESULT 133
LOCUS CF314887 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--03-J15-g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-J15, mRNA sequence.
ACCESSION CF314887
VERSION CF314887.1 GI:33686648
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheng,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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cDNA library (HD)"
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 GCTACGTA 96
Db 2 GCTACGTA 9

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derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
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Db 7 TTTTACT 14

RESULT 133
CF329020
LOCUS
DEFINITION
NACL--04-D03.b1 18 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION
CF329020
VERSION
CF329020.1 GI:33806277
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
|||||
Db 7 TTTTACT 14

RESULT 133
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LOCUS
DEFINITION
NACL--04-D03.b1 18 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--04-D03, mRNA sequence.
ACCESSION
CF329020
VERSION
CF329020.1 GI:33806277
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
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Db 7 TTTTACT 14

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Db 10 TTTTACT 17

RESULT 134
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LOCUS
DEFINITION
NACL--04-N06.b1 18 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION
CF329484
VERSION
CF329484.1 GI:33807207
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 4.8e+07;
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QY 432 TTTTACT 439
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Db 11 TTTTACT 18

RESULT 135
CF329485/c
LOCUS
DEFINITION
NACL--04-N06.g1 18 bp mRNA linear EST 18-AUG-2003
sativa cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION
CF329485
VERSION
CF329485.1 GI:33807209
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 18)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa"
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ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439

Db 8 TTTTACT 1

RESULT 136

CF332520

LOCUS

DEFINITION 18 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--01-A23, mRNA sequence.

ACCESSION

CF332520

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .18

/organism="Oryza sativa"
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cDNA library (JMT)"
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was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96

Db 2 GCTACGTA 9

RESULT 137

CF333354

LOCUS

DEFINITION 18 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--02-D13, mRNA sequence.

ACCESSION

CF333354

VERSION

CF333354.1 GI:33814976

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96

Db 2 GCTACGTA 9

RESULT 138

CF334471

LOCUS

DEFINITION 18 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa cDNA clone JMT--03-M11, mRNA sequence.

ACCESSION

CF334471

VERSION

CF334471.1 GI:33817267

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
 AUTHORS Ehrhartoidae; Oryzae; Oryza.
 1 (bases 1 to 18)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..18
 Location/Qualifiers
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT-03-M1"
 /tissue type="leaf"
 /dev stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96
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 Db 2 GCTACGTA 9

RESULT 139

D11849
 LOCUS HUMM02G05 Liver HepG2 cell line. Homo sapiens cDNA clone hm02g05,
 mRNA sequence.
 DEFINITION 18 bp mRNA linear EST 02-DEC-1992

ACCESSION D11849
 VERSION D11849.1 GI:2155112
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)
 AUTHORS Zukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y.
 and Matsubara, K.

TITLE Large scale cDNA sequencing for analysis of quantitative and
 qualitative aspects of gene expression
 JOURNAL Nat. Genet. 2, 173-179 (1992)
 MEDLINE 94258199
 PUBMED 1345164

COMMENT Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
 Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
 Institute for Molecular and Cellular Biology
 Osaka University
 1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES

source
 1..18
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GBD:D08395E"
 /db_xref="taxon:9606"
 /clone="hm02g05"
 /lab_host="E.coli"

/clone lib="Liver HepG2 cell line."
 /note="3'-directed regional cDNA library. Cleaved by MboI
 and transformed into E.coli."

ORIGIN

Query Match 1.3%; Score 8; DB 14; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 120 ATCCTTTT 127
 |||||
 Db 2 ATCCTTTT 9

RESULT 140

BZ424455/c
 LOCUS BZ424455 18 bp DNA linear GSS 13-DEC-2002
 DEFINITION 10012978-5039 Aspergillus terreus random genomic DNA clone library
 Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424455
 VERSION BZ424455.1 GI:26665910
 KEYWORDS GSS.
 SOURCE Aspergillus terreus

ORGANISM Aspergillus terreus
 Aspergillus terreus
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
 Zimmer, D.P., Boers, M.-E., Blomquist, P.R., Martinez, E.J., Sykes, K.,
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
 Madden, K.T.

TITLE Integrating transcriptional and metabolite profiles to direct the
 engineering of lovastatin-producing strains
 JOURNAL Unpublished (2002)
 COMMENT Contact: Zimmer DP
 Microbia, Inc.
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
 Tel: 617-621-8322
 Fax: 617-

Email: dzimmer@microbia.com
 Class: plasmid ends.

FEATURES

source
 1..18
 Location/Qualifiers
 /organism="Aspergillus terreus"
 /mol_type="genomic DNA"
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"
 /db_xref="taxon:33178"
 /lab_host="Escherichia coli"
 /clone_lib="Aspergillus terreus random genomic DNA clone
 library"
 /note="Vector: pZEXOTM-2; Site1: Sau3A; Site2: BamHI;
 Sau3A genomic fragments ligated into BamHI digested
 pZEXOTM-2 "

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGACGGC 162
 |||||
 Db 8 AGACGGC 1

RESULT 141

BZ424583/c
 LOCUS BZ424583 18 bp DNA linear GSS 13-DEC-2002
 DEFINITION 10015692-4695 Aspergillus terreus random genomic DNA clone library
 Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424583
 VERSION BZ424583.1 GI:26666038
 KEYWORDS GSS.

SOURCE
ORGANISM Aspergillus terreus
Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,
Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,
Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
Madden, K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.

FEATURES
source
1..18
Location/Qualifiers
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZBrOTM-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZBrOTM-2 "
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Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 AGAACGGC 162
| | | | |
DB 8 AGAACGGC 1

RESULT 142
BZ424682/c
LOCUS 18 bp DNA linear GSS 13-DEC-2002
DEFINITION 100017874-4841 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION BZ424682
VERSION BZ424682.1 GI:26666137
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,
Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,
Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
Madden, K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
1..18
Location/Qualifiers

/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZBrOTM-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZBrOTM-2 "
ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 AGAACGGC 162
| | | | |
DB 8 AGAACGGC 1

RESULT 143
BZ424714/c
LOCUS 18 bp DNA linear GSS 13-DEC-2002
DEFINITION 100018520-2995 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
ACCESSION BZ424714
VERSION BZ424714.1 GI:26666169
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,
Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,
Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
Madden, K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.

FEATURES
source
1..18
Location/Qualifiers
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZBrOTM-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZBrOTM-2 "
ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 AGAACGGC 162
| | | | |
DB 8 AGAACGGC 1
RESULT 144

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One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
      Location/Qualifiers
1..18
    /organism="Aspergillus terreus"
    /mol_type="genomic DNA"
    /strain="ATCC 20542 (A. terreus Thom, anamorph)"
    /db_xref="taxon:33178"
    /lab_host="Escherichia coli"
    /clone_lib="Aspergillus terreus random genomic DNA clone
      library"
    /note="Vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;
      Sau3A genomic fragments ligated into BamHI digested
      pZEROTM-2 "

FEATURES             source
Query Match          1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 146	
BZ424914/c	
LOCUS	18 bp DNA
DEFINITION	100021302-5049 Aspergillus terreus random genomic DNA clone library
ACCESSION	Aspergillus terreus genomic, genomic survey sequence.
VERSION	BZ424914
KEYWORDS	BZ424914.1 GI:26666369
SOURCE	GSS.
ORGANISM	Aspergillus terreus
REFERENCE	Aspergillus terreus
AUTHORS	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus; 1 (bases 1 to 18)
	Akenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S., Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J., Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K., Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and Madden, K.T.
TITLE	Integrating transcriptional and metabolite profiles to direct the engineering of lovastatin-producing strains
JOURNAL	Unpublished (2002)
COMMENT	Contact: Zimmer DP

AUTHORS	Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.S., Zimmer, D.P., Boes, M.-G., Blomquist, P.R., Martinez, E.J., Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K., Tobbin, J., Cordero, E., Salama, S.K., Trueheart, J., Royer, J.C. and Madden, K.T.
TITLE	Integrating transcriptional and metabolite profiles to direct the engineering of lovastatin-producing strains
JOURNAL	Unpublished (2002)
COMMENT	Contact: Zimmer DP

Contact: Zimmer Biotech, Inc.
 One Kendall Square Building 1400 W. Cambridge, MA 02139, USA
 Tel: 617-621-8322
 Fax: 617-
 Email: dzimmer@microbia.com
 Class: plasmid ends.
 Location/Qualifiers
 1. .18
 /organism="Aspergillus terreus"
 /mol_type="genomic DNA"
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"
 /db_xref="taxon:33178"
 /ab_host="Escherichia coli"
 /clone_lib="Aspergillus terreus random genomic DNA clone library"
 /note="Vector: pZE-OTM-2; Site 1: Sau3A; Site 2: BamHI; Sau3A genomic fragments ligated into BamHI digested pZEOTM-2"

Query Match 1.3%; Score 8; DB 28; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

FEATURES
 source
 ORIGIN

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QY      155 AGAACGGC 162
      |||||
Db      8 AGAACGGC 1

RESULT 147
BZ425093/c
LOCUS   18 bp DNA linear GSS 13-DEC-2002
DEFINITION
Aspergillus terreus genomic, random genomic DNA clone library
ACCESSION BZ425093
VERSION BZ425093.1 GI:26666548
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 18)
AUTHORS Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
location/Qualifiers
1..18
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZErOTW-2"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      155 AGAACGGC 162
      |||||
Db      8 AGAACGGC 1

RESULT 148
BZ425186/c
LOCUS   18 bp DNA linear GSS 13-DEC-2002
DEFINITION
Aspergillus terreus genomic, random genomic DNA clone library
ACCESSION BZ425186
VERSION BZ425186.1 GI:26666641
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 18)
AUTHORS Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
location/Qualifiers
1..18
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/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZErOTW-2"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      155 AGAACGGC 162
      |||||
Db      8 AGAACGGC 1

RESULT 149
BZ425262/c
LOCUS   18 bp DNA linear GSS 13-DEC-2002
DEFINITION
Aspergillus terreus genomic, random genomic DNA clone library
ACCESSION BZ425262
VERSION BZ425262.1 GI:26666717
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 18)
AUTHORS Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
location/Qualifiers
1..18
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZErOTW-2"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      155 AGAACGGC 162
      |||||
Db      8 AGAACGGC 1

```

```

Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
location/Qualifiers
1..18
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZErOTW-2"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      155 AGAACGGC 162
      |||||
Db      8 AGAACGGC 1

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RESULT 149
BZ425262/c
LOCUS   18 bp DNA linear GSS 13-DEC-2002
DEFINITION
Aspergillus terreus genomic, random genomic DNA clone library
ACCESSION BZ425262
VERSION BZ425262.1 GI:26666717
KEYWORDS GSS.
SOURCE Aspergillus terreus
ORGANISM Aspergillus terreus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
1 (bases 1 to 18)
AUTHORS Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
TITLE Integrating transcriptional and metabolite profiles to direct the
engineering of lovastatin-producing strains
JOURNAL Unpublished (2002)
COMMENT Contact: Zimmer DP
Microbia, Inc.
One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
Tel: 617-621-8322
Fax: 617-
Email: dzimmer@microbia.com
Class: plasmid ends.
FEATURES
source
location/Qualifiers
1..18
/organism="Aspergillus terreus"
/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI;

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ORGANISM      Sau3A genomic fragments ligated into BamHI digested
               pZerOTM-2 "
REFERENCE
AUTHORS       1.3%; Score 8; DB 28; Length 18;
               Best Local Similarity 100.0%; Pred. No. 4.8e+07;
               Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            155 AGAACGGC 162
               |||||
Db            8 AGAACGGC 1
               |||||

RESULT 150
BZ425326/c    18 bp DNA linear GSS 13-DEC-2002
LOCUS
DEFINITION    100029638-4999 Aspergillus terreus random genomic DNA clone library
               Aspergillus terreus genomic, genomic survey sequence.
ACCESSION     BZ425326
VERSION       BZ425326.1 GI:26666781
KEYWORDS      GSS..
SOURCE        Aspergillus terreus
ORGANISM      Aspergillus terreus
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
               Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS       1 (bases 1 to 18)
               Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
               Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
               Monreal,A.W., Feibelman,T.P., Mayoraga,M.E., Maxon,M.E., Sykes,K.,
               Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
               Madden,K.T.
               Integrating transcriptional and metabolite profiles to direct the
               engineering of lovastatin-producing strains
JOURNAL
COMMENT       Unpublished (2002)
               Contact: Zimmer DP
               Microbia, Inc.
               One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
               Tel: 617-621-8322
               Fax: 617-
               Email: dzimmer@microbia.com
               Class: plasmid ends.
FEATURES
source        1..18
               /organism="Aspergillus terreus"
               /mol_type="genomic DNA"
               /strain="ATCC 20542 (A. terreus Thom, anamorph)"
               /db_xref="taxon:33178"
               /lab_host="Escherichia coli"
               /clone_lib="Aspergillus terreus random genomic DNA clone
               library"
               /notes="Vector: pZerOTM-2; Site 1: Sau3A; Site 2: BamHI;
               Sau3A genomic fragments ligated into BamHI digested
               pZerOTM-2 "
ORIGIN
Query Match   1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            155 AGAACGGC 162
               |||||
Db            8 AGAACGGC 1
               |||||

FEATURES
source        1..18
               /organism="Aspergillus terreus"
               /mol_type="genomic DNA"
               /strain="ATCC 20542 (A. terreus Thom, anamorph)"
               /db_xref="taxon:33178"
               /lab_host="Escherichia coli"
               /clone_lib="Aspergillus terreus random genomic DNA clone
               library"
               /notes="Vector: pZerOTM-2; Site 1: Sau3A; Site 2: BamHI;
               Sau3A genomic fragments ligated into BamHI digested
               pZerOTM-2 "
ORGANISM
Query Match   1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            155 AGAACGGC 162
               |||||
Db            8 AGAACGGC 1
               |||||

RESULT 151
BZ425405/c    18 bp DNA linear GSS 13-DEC-2002
LOCUS
DEFINITION    100031360-4855 Aspergillus terreus random genomic DNA clone library
               Aspergillus terreus genomic, genomic survey sequence.
ACCESSION     BZ425405
VERSION       BZ425405.1 GI:26666860
KEYWORDS      GSS..
SOURCE        Aspergillus terreus

```

```

ORGANISM      Aspergillus terreus
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
               Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS       1 (bases 1 to 18)
               Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
               Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
               Monreal,A.W., Feibelman,T.P., Mayoraga,M.E., Maxon,M.E., Sykes,K.,
               Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
               Madden,K.T.
               Integrating transcriptional and metabolite profiles to direct the
               engineering of lovastatin-producing strains
JOURNAL
COMMENT       Unpublished (2002)
               Contact: Zimmer DP
               Microbia, Inc.
               One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
               Tel: 617-621-8322
               Fax: 617-
               Email: dzimmer@microbia.com
               Class: plasmid ends.
FEATURES
source        1..18
               /organism="Aspergillus terreus"
               /mol_type="genomic DNA"
               /strain="ATCC 20542 (A. terreus Thom, anamorph)"
               /db_xref="taxon:33178"
               /lab_host="Escherichia coli"
               /clone_lib="Aspergillus terreus random genomic DNA clone
               library"
               /notes="Vector: pZerOTM-2; Site 1: Sau3A; Site 2: BamHI;
               Sau3A genomic fragments ligated into BamHI digested
               pZerOTM-2 "
ORIGIN
Query Match   1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            155 AGAACGGC 162
               |||||
Db            8 AGAACGGC 1
               |||||

RESULT 152
BZ425442/c    18 bp DNA linear GSS 13-DEC-2002
LOCUS
DEFINITION    100032032-5025 Aspergillus terreus random genomic DNA clone library
               Aspergillus terreus genomic, genomic survey sequence.
ACCESSION     BZ425442
VERSION       BZ425442.1 GI:26666897
KEYWORDS      GSS..
SOURCE        Aspergillus terreus
ORGANISM      Aspergillus terreus
               Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
               Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE
AUTHORS       1 (bases 1 to 18)
               Akenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.,
               Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,E.J.,
               Monreal,A.W., Feibelman,T.P., Mayoraga,M.E., Maxon,M.E., Sykes,K.,
               Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
               Madden,K.T.
               Integrating transcriptional and metabolite profiles to direct the
               engineering of lovastatin-producing strains
JOURNAL
COMMENT       Unpublished (2002)
               Contact: Zimmer DP
               Microbia, Inc.
               One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
               Tel: 617-621-8322
               Fax: 617-
               Email: dzimmer@microbia.com
               Class: plasmid ends.
FEATURES
source        1..18
               /organism="Aspergillus terreus"

```

```

/mol_type="genomic DNA"
/strain="ATCC 20542 (A. terreus Thom, anamorph)"
/db_xref="taxon:33178"
/lab_host="Escherichia coli"
/clone_lib="Aspergillus terreus random genomic DNA clone
library"
/notes="Vector: pZEROM-2; Site_1: Sau3A; Site_2: BamHI;
Sau3A genomic fragments ligated into BamHI digested
pZEROM-2"

ORIGIN
Query Match 1.3%; Score 8; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAAGCGG 162
DB 8 AGAAGCGG 1

RESULT 153
ID HSM007596 standard; mRNA; EST; 19 BP.
XX AC AL042746;
XX SV AL042746.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434C1822_r1 (from clone DKFZp434C1822)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MUPS, Am Klopfferspitze 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1.19
XX FT /db_xref="taxon:9606"
XX FT /mol_type="mRNA"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434C1822"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;

Query Match 1.3%; Score 8; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 CGCGCCGG 398
|||||

```

```

Db 1 CGCGCCGG 8

RESULT 154
LOCUS AA884867
DEFINITION am21b11.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1467453 3' similar to TR:Q93040 Q93040 TIF1BETA ZINC FINGER
PROTEIN. [1] ; mRNA sequence.
ACCESSION AA884867
VERSION AA884867.1 GI:2994848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1216 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1467453"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 1.3%; Score 8; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CGTGACAG 113
|||||
DB 4 CGTGACAG 11

RESULT 155
LOCUS AA885697
DEFINITION cJ34f01.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1500217 3'
similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPF1. [1] ; mRNA
sequence.
ACCESSION AA885697
VERSION AA885697.1 GI:3000805
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 691 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1..19
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1500217"

/tissue_type="carcinoid"

/lab_host="DH10B"

/clone_lib="NCI CGAP Lu5"

/note="Organ: lung; Vector: p77T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PTT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 AATAGCCA 412

|||||

Db 1 AATAGCCA 8

RESULT 156

AA928295/c

LOCUS

DEFINITION AA928295 19 bp mRNA linear EST 22-APR-1998
similar to TR:Q14244 Q14244 MICROBUBULE ASSOCIATED PROTEIN. 1, mRNA sequence.

ACCESSION

AA928295

VERSION

AA928295.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI/MIDR-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Dental Research,

JOURNAL

COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: John Ensley, M.D.

CDNA Library Preparation: Strategene, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1487077"

/tissue_type="squamous cell carcinoma"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="NCI CGAP HN4"

/note="Organ: pharynx; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' (GA)10ACTAGTCGAGTTTTTTTTTTTTTTT 3' "

(GA)10ACTAGTCGAGTTTTTTTTTTTTTTT 3' "

Query Match 1.3%; Score 8; DB 9; Length 19;

Best Local Similarity 100.0%; Pred.No. 4.9e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 GCCCCTGC 261

|||||

Db 18 GCCCCTGC 11

LOCUS AI017940 19 bp mRNA linear EST 27-AUG-1998

cu24b04.x1 Soares NFI.T.GBC.SI Homo sapiens cDNA clone

IMAGE:1627183 3' similar to SW:M94C DROME Q01644 MALE SPECIFIC

SPERM PROTEIN MST84DC. ;contains TAR1.t3 TAR1 repetitive element ;,

mRNA sequence.

ACCESSION AI017940

VERSION AI017940.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1853 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1627183"

/lab_host="DH10B"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /notes="Organ: pooled; Vector: pVT73-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NbH19, testis NHT, and B-cell
 NCI CGAP GCBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 352 GACCGCAA 359

Db 1 GACCGCAA 8

RESULT 158

LOCUS A1122861 19 bp mRNA linear EST 03-SEP-1998
 DEFINITION qb01c07.s1 Soares_pregnant_uterus NbHPU Homo sapiens cDNA clone
 IMAGE:1694988 3' similar to SW:DGK_HUMAN Q16854 DEOXYGUANOSINE
 KINASE PRECURSOR ; mRNA sequence.

ACCESSION A1122861

VERSION A1122861.1 GI:3538627

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant_uterus NbHPU"

/note="Organ: uterus; Vector: pVT73-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pVT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 47 AAAATGTC 54
 |||||
 Db 4 AAAATGTC 11

RESULT 159

A1122861/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant_uterus NbHPU"

/note="Organ: uterus; Vector: pVT73-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pVT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 160

A1476315

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant_uterus NbHPU"

/note="Organ: uterus; Vector: pVT73-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pVT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

Query Match

Best Local Similarity

Matches

Qy

Db

RESULT 160

A1476315

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1694988"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant_uterus NbHPU"

/note="Organ: uterus; Vector: pVT73-Pac; Site_1: Not I;

Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5,

AACTGGAAGATTCCGCCCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pVT73 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 19)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 .AUTHORS
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Mark Raffeld, M.D.
 cDNA Library Preparation: Stratagene, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:204144"
 /tissue_type="follicular lymphoma"
 /lab_host="SOLR (Stratagene, kanamycin resistant)"
 /clone_lib="NCI CGAP_Lym5"
 /note="Organ: lymph node; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.2 kb. Non-amplified library. -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 CCTCGGCC 220

|||||||
 Db 4 CCTCGGCC 11

RESULT 161

AI524591

LOCUS

DEFINITION AI524591 19 bp mRNA linear EST 12-MAY-1999
 similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE
 CHAIN 4 ; mRNA sequence.

ACCESSION

AI524591

VERSION

AI524591.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

.AUTHORS

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 502 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLYA=No.

FEATURES

Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2181833"
 /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ut-4"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

ORIGIN

Query Match 1.3%; Score 8; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CGACTGTG 271

|||||||
 Db 3 CGACTGTG 10

RESULT 162

AI569191/c

LOCUS

DEFINITION AI569191 19 bp mRNA linear EST 14-MAY-1999
 similar to SW:PRCE_HUMAN P28074 PROTEASOME EPSILON CHAIN PRECURSOR
 ; mRNA sequence.

ACCESSION

AI569191

VERSION

AI569191.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

.AUTHORS

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Life Technologies catalog #: 11548-013
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

FEATURES

Location/Qualifiers
 1..19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2224943"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP_Pan1"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"		1.3%; Score 8; DB 9; Length 19; Best Local Similarity 100.0%; Pred.No.4.9e+07; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
ORIGIN		ORIGIN	
Query Match		1.3%; Score 8; DB 9; Length 19;	
Best Local Similarity		100.0%; Pred.No.4.9e+07;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		301 AACCCCAA 308	
Db		12 AACCCCAA 19	
RESULT 164		19 bp mRNA linear EST 16-DEC-1999	
LOCUS		AI683556	
DEFINITION		tx67h08.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2274687 3'	
ACCESSION		AI683556	
VERSION		AI683556.1 GI:4893738	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		1 (bases 1 to 19)	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
JOURNAL		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
COMMENT		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapsb@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	
FEATURES		Trace considered overall poor quality Insert Length: 1385 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers 1..19 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2274687" /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab_host="DH10B" /clone_lib="NCI CGAP Utl1" /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"	
source		ORIGIN	
Query Match		1.3%; Score 8; DB 9; Length 19;	
Best Local Similarity		100.0%; Pred.No.4.9e+07;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		301 AACCCCAA 308	
Db		12 AACCCCAA 19	
RESULT 163		19 bp mRNA linear EST 07-JUN-2001	
LOCUS		AI641650	
DEFINITION		fc22a01.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone	
ACCESSION		IMAGE:3722088 3' similar to TR:Q93107 MYOSIN I HEAVY CHAIN	
VERSION		KINASE.; contains element MSRI repetitive element ;, mRNA sequence.	
KEYWORDS		EST.	
SOURCE		Danio rerio (zebrafish)	
ORGANISM		Danio rerio	
REFERENCE		1 (bases 1 to 19)	
AUTHORS		Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	
TITLE		WashU Zebrafish EST Project 1998	
JOURNAL		Unpublished (1998)	
COMMENT		Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbratfish@wustl.edu cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ReSourceZentrumPrimaDatenbank, Berlin, Germany (web address: www.rzpd.de) Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: T7 ET from Amersham High quality sequence stop: 1. Location/Qualifiers 1..19 /organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:3722088" /sex="mixed" /tissue_type="26 somite embryos, adult livers, shield stage embryos" /lab_host="XLI-blue MRF" /clone_lib="Zebrafish WashU MPIMG EST" /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo (dt)15 primer [5'-pGACTAGTCTTAGTCGCGAGCGCGCCCTTTTCTTTTCTTT3'], double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab, ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST	

Qy	243 CACCTCCT 250
Db	12 CACCTCCT 19
RESULT 165	
AW063940/c	
LOCUS	19 bp mRNA linear EST 07-DEC-2000
DEFINITION	DN0975 KRIBB Human DP Intrathymic T-cell cDNA library Homo sapiens CDNA 3', mRNA sequence.
ACCESSION	AW063940
VERSION	AW063940.1 GI:8887877
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 19) Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C., Park,J.-H., Kim,Y.-S. and Lee,C.-C. Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis Genomics 70 (1), 1-18 (2000) 20541704 PUBMED 11087656 COMMENT Contact: Sung-Ho Goh Genome Center Korea Research Institute of Bioscience and Biotechnology Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea Tel: 82-42-860-4473 Fax: 82-42-860-4479 Email: gohsh@mail.kribb.re.kr Seq primer: T7 High quality sequence stop: 15 POLYA=No.
FEATURES	Location/Qualifiers 1..19 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2821119" /tissue_type="small cell carcinoma" /cell_line="MGC3" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_7" /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACCGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." .
ORIGIN	Query Match 1.3%; Score 8; DB 9; Length 19; Best Local Similarity 100.0%; Pred. No. 4.9e+07; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	343 TTCTGTGA 350
Db	16 TTCTGTGA 9
RESULT 166	
AW248747	
LOCUS	2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.
DEFINITION	mRNA sequence.
ACCESSION	AW248747
VERSION	AW248747.1 GI:6591740
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Other_ESRs: 2821008.5prime Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov
FEATURES	Location/Qualifiers 1..19 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2821119" /tissue_type="small cell carcinoma" /cell_line="MGC3" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_7" /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACCGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." .
ORIGIN	Query Match 1.3%; Score 8; DB 9; Length 19; Best Local Similarity 100.0%; Pred. No. 4.9e+07; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	343 TTCTGTGA 350
Db	16 TTCTGTGA 9
RESULT 167	
AW248820/c	
LOCUS	2821008.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821008 3', mRNA sequence.
DEFINITION	mRNA sequence.
ACCESSION	AW248820
VERSION	AW248820.1 GI:6591813
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Other_ESRs: 2821008.5prime Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov
FEATURES	Location/Qualifiers 1..19 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2821119" /tissue_type="small cell carcinoma" /cell_line="MGC3" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_7" /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACCGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." .
ORIGIN	Query Match 1.3%; Score 8; DB 10; Length 19; Best Local Similarity 100.0%; Pred. No. 4.9e+07; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	429 TTATTITT 436
Db	9 TTATTITT 16
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Other ESrs: 2821008.5prime Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCMS row: L column: 1
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821008"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 AACCCCA 308
| | | | |
Db 16 AACCCCA 9

RESULT 168
AW249918/c
LOCUS
DEFINITION
2821753.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821753 3', mRNA sequence.

ACCESSION
AW249918
VERSION
AW249918.1 GI:6592911
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 19)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821753.5prime
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 11 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: K column: 2
High quality sequence stop: 11.
Location/Qualifiers

FEATURES

source
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821753"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 1.3%; Score 8; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 557 TTGATGAC 564
| | | | |
Db 18 TTGATGAC 11

RESULT 169

CNS08V6Z
LOCUS

DEFINITION
CNS08V6Z
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone FK0AAA44CD05 of strain 6-9 of Anopheles gambiae (African malaria mosquito).

ACCESSION
BX029847
VERSION
BX029847.1 GI:27603128

KEYWORDS
HTC.
SOURCE
Anopheles gambiae (African malaria mosquito)

ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE
1 (bases 1 to 19)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage

JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

FEATURES

source
1..19
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AAA44CD05"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"

ORIGIN

```

Query Match      1.3%; Score 8; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      178 CTCTTCT 185
      |||||
Db      4 CTCTTCT 11

RESULT 170
BM396331
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-2-E02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396331
VERSION     BM396331.1 GI:18196384
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 CTACCGCG 232
      |||||
Db      7 CTACCGCG 14

RESULT 172
BM397831
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-37-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397831
VERSION     BM397831.1 GI:18197884
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      326 TCACCGCG 333
      |||||
Db      7 TCACCGCG 14

RESULT 171
BM396766
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-25-A05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396766
VERSION     BM396766.1 GI:18196819
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)

```

```

COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      225 CTACCGCG 232
      |||||
Db      7 CTACCGCG 14

RESULT 172
BM397831
LOCUS      19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-37-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397831
VERSION     BM397831.1 GI:18197884
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..19
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                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      360 GGCTGAGC 367
      |||||
Db      1 GGCTGAGC 8

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RESULT 173
BM398493
LOCUS
DEFINITION
5009-0-46-A02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM398493
VERSION
BM398493.1 GI:18198546
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
Location/Qualifiers
1..19
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 TCACCGCG 333
|||||
Db 7 TCACCGCG 14

RESULT 174
BM400016
LOCUS
DEFINITION
5009-0-64-G07.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM400016
VERSION
BM400016.1 GI:18200069
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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FEATURES
source
Location/Qualifiers
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/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368
|||||
Db 3 GCTGAGCC 10

RESULT 175
BM401275
LOCUS
DEFINITION
5009-0-85-B03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM401275
VERSION
BM401275.1 GI:18201328
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..19
/organism="Tetrahymena thermophila"
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/strain="CU428.1"
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match 1.3%; Score 8; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GCTGAGCC 368
|||||
Db 2 GCTGAGCC 9

RESULT 176
BQ583648
LOCUS
DEFINITION
E011977-024-005-G09-SP6 MP1Z-ADIS-024-Inflouescence Beta vulgaris
cDNA clone 024-005-G09 5-PRIME, mRNA sequence.
ACCESSION
BQ583648

```

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VERSION BQ583648.1 GI:26113225
SOURCE EST.
ORGANISM Beta vulgaris
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Drungowski, M., Stahl, D., Wruck, W., Hennig, S., Steinfath, M.,
and Radelof, U.
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 5 row: G column: 09
Seq primer: SP6; CATACGATTAGTGACACTATAG.
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:183047"
/db_xref="taxon:161934"
/clone="024-005-G09"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/clone_lib="MPZ-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 199 GACTGGGA 206
|||||
Db 2 GACTGGGA 9
RESULT 177
BQ587387
LOCUS S014305-024-010-H05-SP6 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-010-H05 5-PRIME, mRNA sequence.
ACCESSION BQ587387
VERSION BQ587387.1 GI:26116969
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 5 row: G column: 09
Seq primer: SP6; CATACGATTAGTGACACTATAG.
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/clone="024-005-G09"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/clone_lib="MPZ-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 199 GACTGGGA 206
|||||
Db 2 GACTGGGA 9
RESULT 178
BQ594129/c
LOCUS E012759-024-025-B01-SP6 MPZ-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-025-B01 5-PRIME, mRNA sequence.
ACCESSION BQ594129
VERSION BQ594129.1 GI:26123712
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 10 row: H column: 05
Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
source
1..19
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line)"
/db_xref="GABI:185481"
/db_xref="taxon:161934"
/clone="024-010-H05"
/tissue_type="leaf"
/lab_host="EMDH108"
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 215 CTGGCCGC 222
|||||
Db 8 CTGGCCGC 15
RESULT 178
BQ594129/c
LOCUS E012759-024-025-B01-SP6 MPZ-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-025-B01 5-PRIME, mRNA sequence.
ACCESSION BQ594129
VERSION BQ594129.1 GI:26123712
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 10 row: H column: 05
Seq primer: SP6; CATACGATTAGTGACACTATAG.
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/clone="024-010-H05"
/tissue_type="leaf"
/lab_host="EMDH108"
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/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 215 CTGGCCGC 222
|||||
Db 8 CTGGCCGC 15

```

Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaa@piz-koeln.mpg.de
 Insert Length: 19 Std Error: 0.00
 Plate: 25 row, B column: 01
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

source
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 /issue_type="developing root"
 /lab_host="EMDH108"
 /clone_lib="MPZ-ADIS-024-developing root"
 /note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
 SP6-Sali-CCAGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TTCAGTTC 511
 |||||
 Db 12 TTCAGTTC 5

RESULT 179

EX548528/c
 LOCUS
 DEFINITION BX548528 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse101e02_q1c, mRNA sequence.

ACCESSION BX548528
 VERSION BX548528.1 GI:33298765
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.

REFERENCE

1 (bases 1 to 19)
 LeHane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., LeHane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198

COMMENT

Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike LeHane
 Prof. M.J. LeHane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from

the 3' end.

FEATURES

source
 1. .19
 /organism="Glossina morsitans morsitans"
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 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse101e02_q1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T. brucei"

ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 AGCCCTG 260
 |||||
 Db 17 AGCCCTG 10

RESULT 180

CO1216
 LOCUS
 DEFINITION HUMG30007928 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.

ACCESSION CO1216
 VERSION CO1216.1 GI:1433446
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 19)
 Okubo, K.
 BodyMap: human gene expression database
 Unpublished (1995)
 JOURNAL
 COMMENT

Institute for Molecular and Cellular Biol
 Osaka University
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111 (ex.3315)
 Email: kousaku@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see, http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones represented by this GS sequences is also found there.

FEATURES

source
 1. .19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="Human adult (K.Okubo)"
 /note="One or more human adult tissue"

ORIGIN

Query Match 1.3%; Score 8; DB 13; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCGTG 349
 |||||
 Db 12 CTTCGTG 19

RESULT 181

CO1953/c

LOCUS
DEFINITION HUMGS0004016 Human adult (K.Okubo) mRNA linear EST 31-DEC-2002
sequence.
ACCESSION C01993
VERSION C01993.1 GI:1434223
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Okubo,K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kouaoku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred.No.4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 210 AGACCCCTG 217
|||||
DB 19 AGACCCCTG 12

RESULT 182
C21102/c

LOCUS
DEFINITION C21102 HUMGS0002625 Human adult (K.Okubo) mRNA linear EST 31-DEC-2002
sequence.
ACCESSION C21102
VERSION C21102.1 GI:1622212
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Okubo,K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kouaoku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN
Query Match 1.3%; Score 8; DB 13; Length 19;
Best Local Similarity 100.0%; Pred.No.4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 TGAGGATC 324
|||||
DB 8 TGAGGATC 1

RESULT 183
CA794263/c

LOCUS
DEFINITION CA794263 19 bp mRNA linear EST 05-DEC-2002
Theobroma cacao cDNA clone Cac_BL_1268 5', mRNA sequence.
ACCESSION CA794263
VERSION CA794263.1 GI:26051339
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE 1 (bases 1 to 19)
AUTHORS Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL Planta 216 (2), 255-264 (2002)
MEDLINE 22337596
PUBMED 12447539
COMMENT Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.

FEATURES
source Location/Qualifiers
1..19
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL_1268"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRP"
/clone_lib="Cac BL (Bean and Leaf from Amelonado type
Cacao)"
/note="vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred.No.4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 303 CCCCAACC 310
|||||
DB 16 CCCCAACC 9

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RESULT 184
CA967211/C
LOCUS
DEFINITION
  19 bp mRNA linear EST 03-JAN-2003
  CcLl01a03k1lf2 Carp liver library 1 Cyprinus carpio cDNA clone
  03k11 5', mRNA sequence.
ACCESSION
  CA967211
VERSION
  CA967211.1 GI:27493768
KEYWORDS
  EST.
SOURCE
  Cyprinus carpio (common carp)
  Cyprinus carpio
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE
  1 (bases 1 to 19)
  Gracey,A.Y., Fraser,B., Li,W. and Cossins,A.R.
  Microarray and EST analysis of the carp (Cyprinus carpio)
  transcriptome during environmental stress
  Unpublished (2003)
JOURNAL
  Contact: Andrew R. Cossins
  Laboratory for Environmental Gene Regulation
  University of Liverpool
  School of Biological Sciences, The Biosciences Building, Crown
  Street, Liverpool, United Kingdom, L69 7ZB
  Tel: +44(0)151-795-4510
  Fax: +44(0)151-795-4431
  Email: cossins@liv.ac.uk
  Vector has been trimmed from this EST.
  Plate: 03 row: k column: 11
  Seq primer: Triplex 5' LD (5'-CTCGGAAGCGCGCATTTGTTGGT-3')
  High quality sequence start: 9
  High quality sequence stop: 17.
  Location/Qualifiers
  1..19
  /organism="Cyprinus carpio"
  /mol_type="mRNA"
  /db_xref="taxon:7962"
  /clone="03k11"
  /sex="Male & female"
  /tissue_type="Liver"
  /dev_stage="Adult"
  /lab_host="E.coli Electromax DH10B"
  /clone_lib="Carp liver library 1"
  /notes="Vector: pTriplex2; Site1: sfll GGCATTACGGCC;
  Site 2: sfll GCGCGCTCGGCC; Normalized cDNA library
  prepared from liver of warm, cold and hypoxia challenged
  animals"
FEATURES
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  1..19
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  /mol_type="mRNA"
  /db_xref="taxon:7962"
  /clone="03k11"
  /sex="Male & female"
  /tissue_type="Liver"
  /dev_stage="Adult"
  /lab_host="E.coli Electromax DH10B"
  /clone_lib="Carp liver library 1"
  /notes="Vector: pTriplex2; Site1: sfll GGCATTACGGCC;
  Site 2: sfll GCGCGCTCGGCC; Normalized cDNA library
  prepared from liver of warm, cold and hypoxia challenged
  animals"
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 280 GTGGCCGA 287
  Db 18 GTGGCCGA 11

RESULT 185
CF294232
LOCUS
DEFINITION
  19 bp mRNA linear EST 14-AUG-2003
  30DGS--03-L01.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
  sativa cDNA clone 30DGS--03-L01, mRNA sequence.
ACCESSION
  CF294232
VERSION
  CF294232.1 GI:33663265
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
  Location/Qualifiers
  1..19
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--02-J10"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library I (7LEAF)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
FEATURES
  source
  1..19
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--02-J10"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library I (7LEAF)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 259 TGCTACGA 266
  Db 2 TGCTACGA 9

RESULT 186
CF298891
LOCUS
DEFINITION
  19 bp mRNA linear EST 15-AUG-2003
  7LEAF--02-J10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa cDNA clone 7LEAF--02-J10, mRNA sequence.
ACCESSION
  CF298891
VERSION
  CF298891.1 GI:33670652
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
  Location/Qualifiers
  1..19
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--02-J10"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
FEATURES
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  1..19
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="7LEAF--02-J10"
  /tissue_type="leaf"
  /dev_stage="7 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 259 TGCTACGA 266
  Db 2 TGCTACGA 9

TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
  Location/Qualifiers
  1..19
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="30DGS--03-L01"
  /tissue_type="leaf"
  /dev_stage="30 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
FEATURES
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  1..19
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  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="30DGS--03-L01"
  /tissue_type="leaf"
  /dev_stage="30 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
  /notes="Vector: PCR4-TOPO; Site1: ECORI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."
ORIGIN
  Query Match 1.3%; Score 8; DB 14; Length 19;
  Best Local Similarity 100.0%; Pred. No. 4.9e+07;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 259 TGCTACGA 266
  Db 2 TGCTACGA 9

```

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ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGAGGG 492
|||||
Db 3 GGGAGGG 10

RESULT 187
CF303019
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF1--01-B20.g1 ABF3-overexpressing transgenic rice lambda phage
            cDNA library (ABF1) Oryza sativa cDNA clone ABF1--01-B20, mRNA
            sequence.
ACCESSION  CF303019
VERSION     CF303019.1 GI:33674780
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 19)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES   source
            1..19
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultiivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF1--01-B20"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="ABF3-overexpressing transgenic rice lambda
            phage cDNA library (ABF1)"
            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was dried for 2hrs. cDNA was inserted into_
            lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
            with XhoI site. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCA 497
|||||
Db 12 GGGCTGCA 19

RESULT 188
CF305417
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION CLD1--01-K13.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
            Oryza sativa cDNA clone CLD1--01-K13, mRNA sequence.
ACCESSION  CF305417
VERSION     CF305417.1 GI:33677178
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 19)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES   source
            1..19
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultiivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF1--01-B20"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="ABF3-overexpressing transgenic rice lambda
            phage cDNA library (ABF1)"
            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was dried for 2hrs. cDNA was inserted into_
            lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
            with XhoI site. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTAGAAAA 461
|||||
Db 12 GTAGAAAA 19

RESULT 189
CF306280/c
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION HDAL--03-E08.g1 OSHDAC1-overexpressing transgenic rice lambda phage
            cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-E08, mRNA
            sequence.
ACCESSION  CF306280
VERSION     CF306280.1 GI:33678041
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 19)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES   source
            1..19
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultiivar="Nackdong"
            /db_xref="taxon:4530"
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice cold treated leaf plasmid cDNA library
            (CLD1)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was
            incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
            mRNA was reverse transcribed and then used for PCR."

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTAGAAAA 461
|||||
Db 12 GTAGAAAA 19

RESULT 189
CF306280/c
LOCUS      19 bp mRNA linear EST 15-AUG-2003
DEFINITION HDAL--03-E08.g1 OSHDAC1-overexpressing transgenic rice lambda phage
            cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-E08, mRNA
            sequence.
ACCESSION  CF306280
VERSION     CF306280.1 GI:33678041
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 19)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES   source
            1..19
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultiivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF1--01-B20"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice cold treated leaf plasmid cDNA library
            (CLD1)"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was
            incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
            mRNA was reverse transcribed and then used for PCR."

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1--03-E08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage CDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 CCGCTGGG 61
|||||
Db 12 CCGCTGGG 5

CF306449 19 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HDA1--03-002.g1 OSHDA1-overexpressing transgenic rice lambda phage
CDNA library I (HDA1) Oryza sativa cDNA clone HDAl--03-002, mRNA
sequence.
ACCESSION
CF306449
VERSION
CF306449.1 GI:33678210
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAl--03-002"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred.No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 GCTACGTA 96
|||||
Db 1 GCTACGTA 8

RESULT 192
CF319596/c
LOCUS
DEFINITION
HD-10-C14.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION
CF319596
VERSION
CF319596.1 GI:33691357
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)

```



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ACCESSION      CF340173.1  GI:33828707
VERSION        EST.
KEYWORDS
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     1..19
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="RCL1--07-C20"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E. coli SOLR"
     /clone_lib="Regenerated callus lambda phage cDNA library
               (RCL1)"
     /notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
               XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
               end with SstI and 3' end with XhoI site. Callus was
               induced on 2N6 media for 30 days and cultured for 36hrs on
               regenerated media"

ORIGIN
Query Match      1.3%; Score 8; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 AGTGAAGA 103
|||||
Db 8 AGTGAAGA 15

RESULT 196
CF929669
LOCUS          CF-01-R-E08 Bos taurus CF-24-HW cDNA library Bos taurus cDNA clone
DEFINITION    CF-01-R-E08(5'), mRNA sequence.
ACCESSION     CF929669
VERSION       CF929669.1  GI:38278141
KEYWORDS      EST.
SOURCE        Bos taurus (cow)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
               Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS        Yoon,D.H., Lee,S.H., Lee,J.H., Sang,B.C. and Oh,S.J.
TITLE          Gene Expression Profiling of the Bovine adipose tissues
JOURNAL        Unpublished (2003)
COMMENT        Contact: Dr. Du-Hak Yoon
               National Livestock Research Institute, RDA
               564 Omoekchun-dong, Suwon, 441-350, Korea
               Tel: 82 31 290 1593
               Fax: 82 31 290 1792
               Email: dhyoon@rda.go.kr
               Insert Length: 19 Std Error: 0.00
               Seq primer: ATTAAACCCCTCACTAAG

FEATURES             Location/Qualifiers
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     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC1M0029N17"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 213 CCCTGGCC 220
|||||||
Db 9 CCCTGGCC 2

RESULT 198

AZ315768
LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
1M0033F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0033F01 F, genomic survey sequence.

ACCESSION AZ315768
VERSION AZ315768.1 GI:10362759
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: F column: 01

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0033F01"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TTTCCTTTA 38
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Db 12 TTTCCTTTA 19

RESULT 199

AZ318731
LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
1M0038G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0038G08 F, genomic survey sequence.

ACCESSION AZ318731
VERSION AZ318731.1 GI:10368989
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

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plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: G column: 08

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0038G08"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CTACGTAG 97
|||||||
Db 3 CTACGTAG 10

RESULT 200

AZ318731/c
LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0038G08 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:10368989

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: G column: 08

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

source

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0038G08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CTACGTAG 97
|||||||
Db 10 CTACGTAG 3

RESULT 201

AZ327390
LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0050L09 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:10386092

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0050 row: L column: 09

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0050L09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 TCCTTTTG 543
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Db 1 TCCTTTTG 8

RESULT 202
AZ328922/c
LOCUS
DEFINITION
1M0052L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0052L22 R, genomic survey sequence.

ACCESSION
AZ328922
VERSION
AZ328922.1 GI:10389127
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0052 row: 1 column: 22

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0052L22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 454 GTAGAAAA 461
|||||||
Db 9 GTAGAAAA 2

RESULT 203
AZ329293/c

LOCUS

DEFINITION
1M0053A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0053A03 R, genomic survey sequence.

ACCESSION
AZ329293

VERSION
AZ329293.1 GI:10389864

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0053 row: A column: 03

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0053A03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 AGAAGCTTT 476

Db 9 AGAAGCTTT 2

RESULT 204

AZ345500 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM09080G01F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UUGC1M0080G01 F, genomic survey sequence.

ACCESSION AZ345500

VERSION AZ345500.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: G column: 01

Seq primer: CGTGTGAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080G01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 430 TATTTTAA 437

Db 8 TATTTTAA 15

RESULT 205

AZ345954 19 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM09080G023R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UUGC1M0080G023 R, genomic survey sequence.

ACCESSION AZ345954

VERSION AZ345954.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

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JOURNAL

Unpublished (2000)

COMMENT

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: O column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080G023"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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(http://www.jax.org/resources/documents/dnares/). The DNA

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 GTAGTGAA 101
|||||||
Db 13 GTAGTGAA 6

RESULT 206

AZ346697

LOCUS

DEFINITION AZ346697 19 bp DNA linear GSS 29-SEP-2000
clone UNGC1M082J06 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M082J06"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UNGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 TTTTACT 439
|||||||
Db 2 TTTTACT 9

RESULT 207

AZ358656/c

LOCUS

DEFINITION AZ358656 19 bp DNA linear GSS 02-OCT-2000
clone UUGC1M010K12 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M010K12"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TGTGAGGA 353
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 Db 19 TGTGAGGA 12

RESULT 208

AZ363907
 LOCUS AZ363907 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0109113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0109113 R, genomic survey sequence.

ACCESSION AZ363907
 VERSION AZ363907.1 GI:10477607
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: I column: 13
 Seq primer: CACACGAGAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0109113"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes-vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
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 Db 8 TTATTTT 15

RESULT 209

AZ370656/c
 LOCUS AZ370656 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0121F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0121F18 R, genomic survey sequence.

ACCESSION AZ370656
 VERSION AZ370656.1 GI:10484356
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0121 row: F column: 18
 Seq primer: CACACGAGAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0121F18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes-vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TGGAAATAC 449
|||||||
Db 13 TGGAAATAC 6

RESULT 210

AZ375581

LOCUS

DEFINITION 19 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0129E05 F, genomic survey sequence.

ACCESSION

AZ375581

VERSION

GSS

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

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plasmid inserts

Unpublished (2000)

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University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: E column: 05

Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0129E05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 TTATCTTC 148
|||||||
Db 9 TTATCTTC 16

RESULT 211

AZ387157

LOCUS

DEFINITION

19 bp DNA linear GSS 02-OCT-2000

clone UUGC1M0146E20 R, genomic survey sequence.

ACCESSION

AZ387157

VERSION

GSS

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

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plasmid inserts

Unpublished (2000)

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0146 row: E column: 20

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0146E20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 TTTCCTTA 38
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Db 9 TTTCCTTA 16

RESULT 212

AZ392507
LOCUS
DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UGUC1M0155H11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

US musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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JOURNAL

Unpublished (2000)
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84112, USA

Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0155 row: H column: 11

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGUC1M0155H11"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 ACCTACCT 86
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Db 3 ACCTACCT 10

RESULT 213

AZ393531
LOCUS
DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UGUC1M0156F07 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

US musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weiss, R.

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plasmid inserts

JOURNAL

Unpublished (2000)
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: F column: 07

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGUC1M0156F07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TTTCTTTA 38
|||||||
Db 17 TTTCTTTA 10

RESULT 214
AZ410317/c
LOCUS
DEFINITION
1M0182L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0182L02 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: L column: 02
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0182L02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 479 AAGCCTGG 486
|||||||
Db 9 AAGCCTGG 2

RESULT 215
AZ412553/c

LOCUS
DEFINITION

1M0186M03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0186M03 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: M column: 03
Seg primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186M03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3% Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 CCCCAACC 310
 |||||
 Db 14 CCCCAACC 7

RESULT 216

AZ414372 19 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0188G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0188G18 R, genomic survey sequence.

ACCESSION AZ414372.1 GI:10538385
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0188 row: G column: 18

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0188G18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3% Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTTTACC 40
 |||||
 Db 7 TCTTTACC 14

RESULT 217

AZ424415 19 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0204G02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0204G02 F, genomic survey sequence.

ACCESSION AZ424415
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0204 row: G column: 02

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0204G02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATA 448
|||||||
Db 5 CTGGAATA 12

RESULT 218
AZ424415/c
LOCUS
DEFINITION 1M0204G02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0204G02 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ424415 19 bp DNA linear GSS 03-OCT-2000
1M0204G02F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0204G02 F, genomic survey sequence.
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: G column: 02
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0204G02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 TCCAGACA 524
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Db 9 TCCAGACA 2

RESULT 219
AZ429008/c

LOCUS
DEFINITION 1M0212E07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0212E07 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ429008 19 bp DNA linear GSS 03-OCT-2000
1M0212E07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0212E07 R, genomic survey sequence.
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: E column: 07
Seq primer: CACACAGGAACACGATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0212E07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AATTCAAA 48
 |||||
 Db 16 AATTCAAA 9

RESULT 220
 AZ436629
 LOCUS 19 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0224019F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0224019 F, genomic survey sequence.

ACCESSION AZ436629
 VERSION A2436629.1 GI:10560642
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0224 row: 0 column: 19
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0224019"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTTGATCA 19
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 Db 12 CTTGATCA 19

RESULT 221
 AZ445457

LOCUS

19 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0241J13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0241J13 F, genomic survey sequence.

ACCESSION AZ445457
 VERSION A2445457.1 GI:10595298
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0241 row: J column: 13
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0241J13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 429 TTATTTT 436
|||||||
Db 10 TTATTTT 17

RESULT 222

AZ447252/c

LOCUS

DEFINITION 19 bp DNA linear GSS 04-OCT-2000
1M024M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244M24 F, genomic survey sequence.

ACCESSION

AZ447252

VERSION

A2447252.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: M column: 24

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0244M24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 GGTGATG 562
|||||||
Db 13 GGTGATG 6

RESULT 223

AZ454430

LOCUS

DEFINITION 19 bp DNA linear GSS 04-OCT-2000
1M0256F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0256F21 F, genomic survey sequence.

ACCESSION

AZ454430

VERSION

AZ454430.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

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Unpublished (2000)

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84112, USA

Tel: 801 585 5606

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Insert Length: 10000 Std Error: 0.00

Plate: 0256 row: F column: 21

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0256F21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3% Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 GACTGGGA 206
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Db 5 GACTGGGA 12

RESULT 224
AZ475705/c
LOCUS
DEFINITION
1M0294B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0294B02 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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JOURNAL

COMMENT

Unpublished (2000)
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84112, USA

Tel: 801 585 5606
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Email: dduun@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0294 row: B column: 02

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0294B02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3% Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AGCCTGGG 487
|||||||
Db 18 AGCCTGGG 11

RESULT 225
AZ484016/c

LOCUS

DEFINITION
1M0310J10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0310J10 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
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Tel: 801 585 5606

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Email: dduun@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0310 row: J column: 10

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0310J10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 TTGGTTAT 144
|||||||
Db 8 TTGGTTAT 1

RESULT 226

AZ484528

LOCUS

DEFINITION 1M0311J03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0311J03 F, genomic survey sequence.

ACCESSION

AZ484528

VERSION

AZ484528.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0311 row: J column: 03

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0311J03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGGGCTAA 65
|||||||
Db 3 TGGGCTAA 10

RESULT 227

AZ485264/c

LOCUS

DEFINITION 1M0312002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0312002 R, genomic survey sequence.

ACCESSION

AZ485264

VERSION

AZ485264.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0312 row: O column: 02

Seq primer: CACACAGGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0312002"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 CACCTCCT 250
|||||||
Db 8 CACCTCCT 1

RESULT 228
AZ493833/c
LOCUS
DEFINITION
1M0328P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328P11 R, genomic survey sequence.

ACCESSION
AZ493833
VERSION
AZ493833.1 GI:10667884
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
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plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0328 row: P column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0328P11"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 CCCCAACC 310
|||||||
Db 15 CCCCAACC 8

RESULT 229
AZ495849/c

LOCUS

DEFINITION
1M0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0331N22 R, genomic survey sequence.

ACCESSION
AZ495849
VERSION
AZ495849.1 GI:10671571
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
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84112, USA

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0331 row: N column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0331N22"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|G|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 480 AGCCTGGG 487
|||||||
Db 8 AGCCTGGG 1

RESULT 230
AZ507472/c
LOCUS
DEFINITION
1M0349D11f Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0349D11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ507472 19 bp DNA linear GSS 05-OCT-2000
1M0349D11f Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0349D11 F, genomic survey sequence.
AZ507472
AZ507472.1 GI:10688788
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
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Unpublished (2000)
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0349 row: D column: 11
Seq primer: CGTTGTAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0349D11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

FEATURES
source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0349D11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 CAAGGCTG 364
|||||||
Db 12 CAAGGCTG 5

RESULT 231
AZ514386

LOCUS
DEFINITION
1M0361H02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0361H02 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ514386 19 bp DNA linear GSS 05-OCT-2000
1M0361H02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0361H02 F, genomic survey sequence.
AZ514386
AZ514386.1 GI:10695702
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 02
Seq primer: CGTTGTAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0361H02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

FEATURES
source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0361H02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 ACAGTGCT 117
 |||||
 Db 1 ACAGTGCT 8

RESULT 232
 AZ514722/c
 LOCUS
 DEFINITION
 1M0361C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0361C10 R, genomic survey sequence.

ACCESSION
 AZ514722
 VERSION
 AZ514722.1 GI:10696038
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: C column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0361C10"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 CAAAAATG 52
 |||||
 Db 18 CAAAAATG 11

RESULT 233

AZ514774

LOCUS

DEFINITION
 1M0361N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0361N11 R, genomic survey sequence.

ACCESSION
 AZ514774

VERSION
 AZ514774.1 GI:10696090

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: N column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0361N11"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 338 TCTACTTC 345
 |||||
 Db 6 TCTACTTC 13

RESULT 234
 AZ579084
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0363M07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0363M07 F, genomic survey sequence.

ACCESSION AZ579084
 VERSION AZ579084.1 GI:11693545
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0363 row: M column: 07
 Seg primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0363M07"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 492 GCTGCATG 499
 |||||
 Db 5 GCTGCATG 12

RESULT 235
 AZ581123
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0365N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0365N08 R, genomic survey sequence.

ACCESSION AZ581123
 VERSION AZ581123.1 GI:11695820
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0369 row: N column: 08
 Seg primer: CACACGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
 source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0365N08"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 114 TGCTACAT 121
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 Db 12 TGCTACAT 19

RESULT 236
 AZ585820
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0391115F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391115 F, genomic survey sequence.
 ACCESSION AZ585820
 VERSION AZ585820.1 GI:11708010
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0391 row: I column: 15
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0391115"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
 source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 360 GGCTGAGC 367
 |||||
 Db 10 GGCTGAGC 17

RESULT 237
 AZ586377/c
 LOCUS 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0392A15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0392A15 F, genomic survey sequence.
 ACCESSION AZ586377
 VERSION AZ586377.1 GI:11708567
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0392 row: A column: 15
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0392A15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
 source

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 TGCAATA 408
|||||||
Db 15 TGCAATA 8

RESULT 238

AZ588155
LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0396110F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0396110 F, genomic survey sequence.

ACCESSION AZ588155
VERSION 1
KEYWORDS GSS.
SOURCE 1 GI:11710261

Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0396 row: 1 column: 10
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0396110"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 AAAAATGT 53
|||||||
Db 3 AAAAATGT 10

RESULT 239

AZ591963
LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0402P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0402P23 F, genomic survey sequence.

ACCESSION AZ591963
VERSION 1
KEYWORDS GSS.
SOURCE 1 GI:11714153

Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: P column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0402P23"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 ATTGCTCT 181
|||||
Db 8 ATTGCTCT 15

RESULT 240

AZ610451 19 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
M0435C198 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0435C18 R, genomic survey sequence.

ACCESSION
AZ610451

VERSION
AZ610451.1 GI:11732641

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0435 row: C column: 18

Seq primer: CACACAGGAAACACCTATGACC

Class: Plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0435C18"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 GCGGCTG 387
|||||
Db 7 GCGGCTG 14

RESULT 241

AZ611716 19 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
M0439B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0439B15 F, genomic survey sequence.

ACCESSION
AZ611716

VERSION
AZ611716.1 GI:11733906

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0438 row: B column: 15

Seq primer: CTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0439B15"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 CGCGCGCC 337
|||||
Db 11 CGCGCGCC 4

RESULT 242

AZ623283
LOCUS
DEFINITION
1M0460N18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460N18 R, genomic survey sequence.

ACCESSION
AZ623283
VERSION
AZ623283.1 GI:11745473
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: N column: 18

Seq primer: CACACAGGAACGATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460N18"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 CACCTGGT 241
|||||
Db 2 CACCTGGT 9

RESULT 243

AZ626685/c

LOCUS

DEFINITION
1M0467M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0467M01 F, genomic survey sequence.

ACCESSION
AZ626685
VERSION
AZ626685.1 GI:11748875
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0467 row: M column: 01

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0467M01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 GAAGGGCT 494
|||||||
Db 19 GAAGGGCT 12

RESULT 244
AZ654747
LOCUS
DEFINITION
1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529F08 F, genomic survey sequence.

ACCESSION
AZ654747
VERSION
AZ654747.1 GI:11791893
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

University of Utah
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: F column: 08

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES
source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529F08"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436
|||||||
Db 4 TTATTTT 11

RESULT 245

AZ655467

LOCUS

DEFINITION
1M0530O17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0530O17 F, genomic survey sequence.

ACCESSION
AZ655467

VERSION
AZ655467.1 GI:11792529

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rielly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

University of Utah
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0530 row: O column: 17

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES
source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0530O17"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 GGCTGAGC 367
 |||||
 Db 10 GGCTGAGC 17

RESULT 246
 AZ655467/c
 LOCUS
 DEFINITION 1M0530017F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0530017 F, genomic survey sequence.

ACCESSION AZ655467
 VERSION AZ655467.1 GI:11792529
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0530 row: 0 column: 17
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
source

1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0530017"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 AGGCATCA 415
 |||||
 Db 13 AGGCATCA 6

RESULT 247
 AZ655870/c
 LOCUS
 DEFINITION 1M0531N06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0531N06 F, genomic survey sequence.

ACCESSION AZ655870
 VERSION AZ655870.1 GI:11793016
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0531 row: N column: 06
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
source

1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0531N06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G14732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 AGTCTGAG 320
 |||||
 Db 17 AGTCTGAG 10

RESULT 248
AZ658087/c

LOCUS
 DEFINITION 1M0534J09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0534J09 R, genomic survey sequence.

ACCESSION AZ658087
 VERSION AZ658087.1 GI:11795233
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: J column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0534J09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G14732114|9b|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 TCTGTGAG 351
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 Db 13 TCTGTGAG 6

RESULT 249
AZ664265/c

LOCUS
 DEFINITION 1M0544A19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0544A19 F, genomic survey sequence.

ACCESSION AZ664265
 VERSION AZ664265.1 GI:11801411
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.

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JOURNAL

Unpublished (2000)

COMMENT

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0544 row: A column: 19

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGC 178
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Db 8 GGAATTGC 1

RESULT 250

AZ759944
LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0553010F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0553010 F, genomic survey sequence.

ACCESSION AZ759944
VERSION AZ759944.1 GI:12867253
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

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Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: 0 column: 10

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0553010"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GGAGGAAG 30
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Db 4 GGAGGAAG 11

RESULT 251

AZ759944/c
LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0553010F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0553010 F, genomic survey sequence.

ACCESSION AZ759944
VERSION AZ759944.1 GI:12867253
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

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Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: 0 column: 10

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0553010"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCCCTCC 187
 |||||
 Db 11 CTTCCCTCC 4

RESULT 252
 AZ764662/c
 LOCUS
 DEFINITION 19 bp DNA linear GSS 16-FEB-2001
 IM0561K11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0561K11 F, genomic survey sequence.

ACCESSION
 AZ764662
 VERSION
 AZ764662.1 GI:12879855
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A., and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0561 row: K column: 11
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0561K11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AGGGGCTG 378
 |||||
 Db 19 AGGGGCTG 12

RESULT 253
 AZ769438

LOCUS
 DEFINITION 19 bp DNA linear GSS 16-FEB-2001
 IM0570P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0570P09 F, genomic survey sequence.

ACCESSION
 AZ769438
 VERSION
 AZ769438.1 GI:12889573
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A., and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0570 row: F column: 09
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0570P09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
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 (http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 ATTCAAAA 49
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Db 5 ATTCAAAA 12

RESULT 254
AZ772446 19 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0583016F Mouse 10kb plasmid UUGCJM library Mus musculus genomic
DEFINITION clone UUGCJM0583016 F, genomic survey sequence.

ACCESSION AZ772446
VERSION AZ772446.1 GI:12895762
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
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University of Utah
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0583 row: 0 column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCJM0583016"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCJM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 TGACAGTG 115
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Db 9 TGACAGTG 16

RESULT 255
AZ778302/c

LOCUS AZ778302 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0013C02F Mouse 10kb plasmid UUGCJM library Mus musculus genomic
clone UUGC2M0013C02 F, genomic survey sequence.

ACCESSION AZ778302
VERSION AZ778302.1 GI:12907800
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0013 row: C column: 02

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0013C02"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCJM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 GTAGTGAA 101
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 Db 10 GTAGTGAA 3

RESULT 256
 AZ778801/c
 LOCUS
 DEFINITION
 2M0014013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0014013 F, genomic survey sequence.

ACCESSION
 AZ778801
 VERSION
 AZ778801.1 GI:12908811
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UUGC2M0014013"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
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 (http://www.jax.org/resources/documents/dnares/). The DNA
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FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /clone="UUGC2M0014013"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
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 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TTCAGTTC 511
 |||||
 Db 17 TTCAGTTC 10

RESULT 257
 AZ783702
 LOCUS
 DEFINITION
 2M0025108R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0025108 R, genomic survey sequence.

ACCESSION
 AZ783702
 VERSION
 AZ783702.1 GI:12918705
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 DUNN,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0025 row: 1 column: 08
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0025108"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0025108"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 ACTGTGCC 273

Db |||||

2 ACTGTGCC 9

RESULT 258

AZ784693

LOCUS

DEFINITION AZ784693 19 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0027N18 R, genomic survey sequence.

ACCESSION

AZ784693

VERSION

GI:12920689

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: N column: 18
Seq primer: CACACAGAAACGATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0027N18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 GTGCAAT 407

Db |||||

12 GTGCAAT 19

RESULT 259

AZ787588/c

LOCUS

DEFINITION AZ787588 19 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0034A07 F, genomic survey sequence.

ACCESSION

AZ787588

VERSION

GI:12926529

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE

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plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: A column: 07
Seq primer: CGTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 GTTCTTTT 37
|||||||
Db 8 GTTCTTTT 1

RESULT 260

AZ789674
LOCUS
DEFINITION 2M0037L08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCG2M0037L08 R, genomic survey sequence.

ACCESSION AZ789674
VERSION AZ789674.1 GI:12930742
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0037 row: L column: 08

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0037L08"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 TTATTTT 436
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Db 12 TTATTTT 19

RESULT 261

AZ792828
LOCUS
DEFINITION 2M0045N01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCG2M0045N01 R, genomic survey sequence.

ACCESSION AZ792828
VERSION AZ792828.1 GI:12937159
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: N column: 01

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0045N01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGGCTGA 365
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DB 11 AAGGCTGA 4

RESULT 262

AZ794641
LOCUS
DEFINITION 2M0048E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0048E05 R, genomic survey sequence.

ACCESSION AZ794641
VERSION
KEYWORDS
SOURCE GSS.
GI:12940815

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: E column: 05
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0048E05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 CTGCTGGA 445
|||||
DB 10 CTGCTGGA 17

RESULT 263

AZ795136/c
LOCUS
DEFINITION 2M0049A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0049A16 F, genomic survey sequence.

ACCESSION AZ795136
VERSION
KEYWORDS
SOURCE GSS.
GI:12941845

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: A column: 16
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0049A16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 TGCTACAT 121
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Db 14 TGCTACAT 7

RESULT 264
AZ798955/c
LOCUS
DEFINITION
2M0056K01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0056K01 F, genomic survey sequence.

ACCESSION
AZ798955
VERSION
AZ798955.1 GI:12949578
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
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plasmid inserts

JOURNAL

COMMENT
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: K column: 01

Seq primer: CGTTGTAACACGACGCGCACT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056K01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AAGTTTCT 35
|||||||
Db 8 AAGTTTCT 1

RESULT 265
AZ800056

LOCUS
DEFINITION
2M0057E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0057E20 R, genomic survey sequence.

ACCESSION
AZ800056
VERSION
AZ800056.1 GI:12951797
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0057 row: E column: 20

Seq primer: CACACAGCAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0057E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 TGCTGGAA 446
|||||||
Db 3 TGCTGGAA 10

RESULT 266

AZ804026/c

LOCUS

DEFINITION AZ804026 19 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0064007 R, genomic survey sequence.

ACCESSION

AZ804026

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: 0 column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0064007"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 TTCAGTTC 511
|||||||
Db 17 TTCAGTTC 10

RESULT 267

AZ805995

LOCUS

DEFINITION AZ805995 19 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0067F13 R, genomic survey sequence.

ACCESSION

AZ805995

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0067 row: F column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0067F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

FEATURES

source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 TTTCTGGC 296
|||||||
Db 3 TTTCTGGC 10

RESULT 268

AZ807749
LOCUS 2M0070L17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0070L17 R, genomic survey sequence.

ACCESSION AZ807749
VERSION 1
KEYWORDS GI:12972406
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: L column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0070L17"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 CCTGGAGC 255
|||||||
Db 12 CCTGGAGC 19

RESULT 269

AZ810098
LOCUS 2M0074N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0074N21 F, genomic survey sequence.

ACCESSION AZ810098
VERSION 1
KEYWORDS GI:12977022
SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: N column: 21

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074N21"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 CCCTGCTA 263
|||||||
Db 12 CCCTGCTA 19

RESULT 270

AZ811522 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0077M12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0077M12 R, genomic survey sequence.

ACCESSION AZ811522
VERSION AZ811522.1 GI:12979860
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: M column: 12
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
1..19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0077M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGC 441
|||||||
Db 7 TTTACTGC 14

RESULT 271

AZ813099 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0080P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0080P09 F, genomic survey sequence.

ACCESSION AZ813099
VERSION AZ813099.1 GI:12983007
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0080P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 CGCAATAA 155
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DB 13 CGCAATAA 6

RESULT 272

AZ815827/c 19 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0084K23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0084K23 F, genomic survey sequence.

ACCESSION AZ815827
VERSION AZ815827.1 GI:12985735
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: K column: 23
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0084K23"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 ATGACCTT 422
|||||
DB 17 ATGACCTT 10

RESULT 273

AZ816318 19 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0085E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0085E05 F, genomic survey sequence.

ACCESSION AZ816318
VERSION AZ816318.1 GI:12986226
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: E column: 05
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0085E05"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 AACGGCTG 164
|||||||
Db 6 AACGGCTG 13

RESULT 274

AZ820818 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M00931118F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M00931118 F, genomic survey sequence.

ACCESSION AZ820818
VERSION AZ820818.1 GI:12990726
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

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JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0093 row: 1 column: 18

Seq primer: CGTTGTAAACACGCCCGCAT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC2M0093118"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 ACCCTGGC 219
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Db 10 ACCCTGGC 17

RESULT 275

AZ822457 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0095D16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0095D16 R, genomic survey sequence.

ACCESSION AZ822457
VERSION AZ822457.1 GI:12992365
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0095 row: D column: 16

Seq primer: CACACAGGAACACGATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0095D16"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 504 TTCAGTTC 511
|||||||
Db 9 TTCAGTTC 2

RESULT 276

AZ8271164/c
LOCUS
DEFINITION
2M0103M22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103M22 F, genomic survey sequence.

ACCESSION
AZ8271164
VERSION
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 19)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: M column: 22
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103M22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 456 AGAAACC 463
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Db 14 AGAAACC 7

RESULT 277

AZ830469
LOCUS
DEFINITION
2M0109C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0109C14 R, genomic survey sequence.

ACCESSION
AZ830469
VERSION
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 19)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: C column: 14
Seq primer: CACACAGCAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. .19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0109C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 TGGGACCT 209
|||||||
Db 4 TGGGACCT 11

RESULT 278
AZ834391
LOCUS
DEFINITION
2M0117N04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0117N04 F, genomic survey sequence.

ACCESSION
AZ834391
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: N column: 04
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0117N04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCITTACC 40
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Db 5 TCITTACC 12

RESULT 279
AZ835621
LOCUS
DEFINITION
2M0129L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0129L21 R, genomic survey sequence.

ACCESSION
AZ835621
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: L column: 21
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0129L21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTCTGTGA 350
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Db 2 TTCTGTGA 9

RESULT 280

AZ839642
LOCUS 2M0135C33R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0135C23 R, genomic survey sequence.

ACCESSION AZ839642
VERSION 1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0135 row: C column: 23

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0135C23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GGCGTGAG 78
|||||||
Db 5 GGCGTGAG 12

RESULT 281

AZ841926
LOCUS 2M0140K06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0140K06 F, genomic survey sequence.

ACCESSION AZ841926
VERSION 1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0140 row: K column: 06

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0140K06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 AAGGCTGA 365
|||||||
Db 7 AAGGCTGA 14

RESULT 282

AZ858730
LOCUS
DEFINITION 2M0164104F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0164104 F, genomic survey sequence.

ACCESSION AZ858730
VERSION
KEYWORDS
SOURCE

US musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0164 row: 1 column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0164104"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 GCCGCTGC 225
|||||||
Db 5 GCCGCTGC 12

RESULT 283

AZ858730/c
LOCUS
DEFINITION 2M0164104F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0164104 F, genomic survey sequence.

ACCESSION AZ858730
VERSION
KEYWORDS
SOURCE

US musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0164 row: 1 column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0164104"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 CAAGGCTG 364
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Db 19 CAAGGCTG 12

RESULT 284

AZ862758
LOCUS 2M0170005R Mouse 10kb plasmid UUGCJM library Mus musculus genomic
DEFINITION clone UUGC2M0170005 R, genomic survey sequence.

ACCESSION AZ862758
VERSION AZ862758.1 GI:13060381
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0170 row: 0 column: 05

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0170005"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCJM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 ATTCAAAA 49
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Db 12 ATTCAAAA 19

RESULT 285

AZ862767
LOCUS 2M0170A03R Mouse 10kb plasmid UUGCJM library Mus musculus genomic
DEFINITION clone UUGC2M0170A09 R, genomic survey sequence.

ACCESSION AZ862767
VERSION AZ862767.1 GI:13060399
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0170 row: A column: 09

Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 19.
Location/Qualifiers

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0170A09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCJM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 CACTGGAC 135
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Db 10 CACTGGAC 17

RESULT 286
AZ875430/c

LOCUS AZ875430 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0189K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0189K09 R, genomic survey sequence.

ACCESSION AZ875430
VERSION AZ875430.1 GI:13085433
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0189 row: K column: 09

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

1. .19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0189K09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CCTCAGTC 316
|||||||
Db 18 CCTCAGTC 11

RESULT 287
AZ942806/c

LOCUS AZ942806 19 bp DNA linear GSS 26-APR-2001
DEFINITION 2M0203F09F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203F09 F, genomic survey sequence.

ACCESSION AZ942806
VERSION AZ942806.1 GI:13806397
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: F column: 09

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

1. .19
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0203F09"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 581 GTACTTTG 588
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 Db 16 GTACTTTG 9

RESULT 288

AZ960826
 LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0229H03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0229H03 F, genomic survey sequence.

ACCESSION AZ960826
 VERSION AZ960826.1 GI:13832053

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0229 row: H column: 03

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0229H03"
 /sex="Female"

/lab_hosts="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 ATTCAAAA 49
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 Db 3 ATTCAAAA 10

RESULT 289

AZ960826/c
 LOCUS 19 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0229H03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0229H03 F, genomic survey sequence.

ACCESSION AZ960826
 VERSION AZ960826.1 GI:13832053

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0229 row: H column: 03

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
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 /sex="Female"

/lab_hosts="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 447 TACTTTTG 454
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 Db 13 TACTTTTG 6

RESULT 290

AZ967656
 LOCUS 2M0238M09R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION Clone UUGC2M0238M09 R, genomic survey sequence.

ACCESSION AZ967656
 VERSION AZ967656.1 GI:13838883
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0238 row: M column: 09
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0238M09"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 CAAAAATG 52
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 Db 2 CAAAAATG 9

RESULT 291

AZ977761/c
 LOCUS 2M0253I16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION Clone UUGC2M0253I16 R, genomic survey sequence.

ACCESSION AZ977761
 VERSION AZ977761.1 GI:13848988
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0253 row: I column: 16
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source
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 /db_xref="taxon:10090"
 /clone="UUGC2M0253I16"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

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ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 TTGTGTAGA 458
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Db 15 TTGTGTAGA 8

RESULT 292

AZ983624

LOCUS AZ983624 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0264A22R Mouse 10kb plasmid UGC2M library Mus musculus genomic
clone UGC2M0264A22 R, genomic survey sequence.

ACCESSION AZ983624

VERSION AZ983624.1

GI:113854851

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0264 row: A column: 22

Seq primer: CACACGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0264A22"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 141 TTATCTTC 148
|||||
Db 8 TTATCTTC 15

RESULT 293

AZ989738/c

LOCUS AZ989738 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0273M10F Mouse 10kb plasmid UGC2M library Mus musculus genomic
clone UGC2M0273M10 F, genomic survey sequence.

ACCESSION AZ989738

VERSION AZ989738.1

GI:13860965

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: M column: 10

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0273M10"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTT 435
|||||
Db 8 ATTATTTT 1

RESULT 294
AZ990193/c
LOCUS
DEFINITION
2M0273L15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0273L15 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: L column: 15
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0273L15"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGGGAAGG 492
|||||
Db 15 GGGGAAGG 8

RESULT 295
BH000440/c

LOCUS
DEFINITION
2M0288I117F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288I117 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: I column: 17
Seq primer: CGTTGTTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288I17"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.9e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 AACTTCA 478

Db 15 AACTTCA 8

RESULT 296

BZ424622 19 bp DNA linear GSS 13-DEC-2002
LOCUS
DEFINITION 10016863-4991 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424622

VERSION BZ424622.1

KEYWORDS GI:26666077

SOURCE GSS.

ORGANISM Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,

Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,

Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,

Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and

Madden, K.T.

Integrating transcriptional and metabolite profiles to direct the

engineering of lovastatin-producing strains

Unpublished (2002)

Contact: Zimmer DP

Microbia, Inc.

Tel: 617-621-8322

Fax: 617-

Email: dzimmer@microbia.com

Class: plasmid ends.

Location/Qualifiers

1. .19

/organism="Aspergillus terreus"

/mol_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db_xref="taxon:33178"

/lab_host="Escherichia coli"

/clone_lib="Aspergillus terreus random genomic DNA clone

library"

/note="vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;

Sau3A genomic fragments ligated into BamHI digested

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

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pZEROTM-2"

Db

9 AGAACGGC 2

RESULT 297

BZ424949/c

LOCUS

DEFINITION

100022331-5019 Aspergillus terreus random genomic DNA clone library

Aspergillus terreus genomic, genomic survey sequence.

ACCESSION BZ424949

VERSION BZ424949.1

KEYWORDS GI:26666404

SOURCE GSS.

ORGANISM Aspergillus terreus

Aspergillus terreus

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,

Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,

Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,

Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and

Madden, K.T.

Integrating transcriptional and metabolite profiles to direct the

engineering of lovastatin-producing strains

Unpublished (2002)

Contact: Zimmer DP

Microbia, Inc.

Tel: 617-621-8322

Fax: 617-

Email: dzimmer@microbia.com

Class: plasmid ends.

Location/Qualifiers

1. .19

/organism="Aspergillus terreus"

/mol_type="genomic DNA"

/strain="ATCC 20542 (A. terreus Thom, anamorph)"

/db_xref="taxon:33178"

/lab_host="Escherichia coli"

/clone_lib="Aspergillus terreus random genomic DNA clone

library"

/note="vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;

Sau3A genomic fragments ligated into BamHI digested

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

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pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

pZEROTM-2"

engineering of lovastatin-producing strains
 Unpublished (2002)
 Contact: Zimmer DP
 Microbia, Inc.
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
 Tel: 617-621-8322
 Fax: 617-
 Email: dzimmer@microbia.com
 Class: plasmid ends.

FEATURES

source
 1..19
 /organism="Aspergillus terreus"
 /mol_type="genomic DNA"
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"
 /db_xref="taxon:33178"
 /lab_host="Escherichia coli"
 /clone_lib="Aspergillus terreus random genomic DNA clone library"
 /note="Vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;
 Sau3A genomic fragments ligated into BamHI digested
 pZEROTM-2 "

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 155 AGAACGGC 162
 Db 8 AGAACGGC 1

RESULT 299

BZ425408/c
 LOCUS BZ425408 19 bp DNA linear GSS 13-DEC-2002
 DEFINITION 100031441-5051 Aspergillus terreus random genomic DNA clone library
 Aspergillus terreus genomic, genomic survey sequence.
 ACCESSION BZ425408
 VERSION BZ425408.1 GI:26666863
 KEYWORDS GSS.
 SOURCE Aspergillus terreus
 ORGANISM Aspergillus terreus
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE

1 (bases 1 to 19)
 Akenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S.,
 Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J.,
 Monreal, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K.,
 Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
 Madden, K.T.
 Integrating transcriptional and metabolite profiles to direct the
 engineering of lovastatin-producing strains

TITLE

Unpublished (2002)
 Contact: Zimmer DP
 Microbia, Inc.
 One Kendall Square Building 1400 W, Cambridge, MA 02139, USA
 Tel: 617-621-8322
 Fax: 617-
 Email: dzimmer@microbia.com
 Class: plasmid ends.

FEATURES

source
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 /organism="Aspergillus terreus"
 /mol_type="genomic DNA"
 /strain="ATCC 20542 (A. terreus Thom, anamorph)"
 /db_xref="taxon:33178"
 /lab_host="Escherichia coli"
 /clone_lib="Aspergillus terreus random genomic DNA clone library"
 /note="Vector: pZEROTM-2; Site 1: Sau3A; Site 2: BamHI;
 Sau3A genomic fragments ligated into BamHI digested
 pZEROTM-2 "

ORIGIN

Query Match 1.3%; Score 8; DB 28; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 155 AGAACGGC 162
 Db 8 AGAACGGC 1

RESULT 300

TA30B01Q/c
 LOCUS TA30B01Q 19 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 30b01, reverse sequence,
 genomic survey sequence.
 ACCESSION AL452860
 VERSION AL452860.1 GI:11854424
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE

1 (bases 1 to 19)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

Email: neisayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
 1..19
 /organism="Trypanosoma brucei"
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 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="30b01"

ORIGIN

Query Match 1.3%; Score 8; DB 29; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.9e+07;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 GAAGTTTC 34
 Db 18 GAAGTTTC 11

Search completed: March 4, 2004, 23:31:52
 Job time : 2297 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 4, 2004, 23:34:18 ; Search time 3736 Seconds
(without alignments)
2297.088 Million cell updates/sec

Title: US-09-966-880A-8
Perfect score: 198
Sequence: 1 MDSLLMNRKFLYQFNVRW.....ILLPLYEVDDLRDAFRUGL 198

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 1

Total number of hits satisfying chosen parameters: 687819

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US09966880/runat_04032004_083152_22387/app.query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPEL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=300 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20
-USER=US09966880@cgn.1.1.3731@runat_04032004_083152_22387 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
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24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*

29: em.vi.*
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31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
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35: em.htg.rod.*
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37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	6	3.0	18	6	AR300029	Sequence
C 2	6	3.0	19	6	AR295883	Sequence
3	6	3.0	20	6	AR026495	Sequence
C 4	6	3.0	20	6	AR224722	Sequence
5	6	3.0	20	6	AR297575	Sequence
6	6	3.0	20	6	AR314839	Sequence
7	5	2.5	15	6	AR180659	Sequence
C 8	5	2.5	16	6	AX322719	Sequence
9	5	2.5	17	6	A35587	A35587 Synthetic h
C 10	5	2.5	17	6	A45700	A45700 Sequence 31
C 11	5	2.5	17	6	AR039735	Sequence
C 12	5	2.5	17	6	AR039737	Sequence
13	5	2.5	17	6	AR057431	Sequence
14	5	2.5	17	6	AR057487	Sequence
15	5	2.5	17	6	AR057687	Sequence
16	5	2.5	17	6	AR057777	Sequence
17	5	2.5	17	6	AR057782	Sequence
18	5	2.5	17	6	AR115189	Sequence
19	5	2.5	17	6	AR115245	Sequence
20	5	2.5	17	6	AR115445	Sequence
21	5	2.5	17	6	AR115535	Sequence
22	5	2.5	17	6	AR115540	Sequence
23	5	2.5	17	6	BD241216	BD241216 Methods a
C 24	5	2.5	17	6	BD256674	BD256674 Regulatio
25	5	2.5	17	6	AR186522	Sequence
26	5	2.5	17	6	AR186523	Sequence
27	5	2.5	17	6	AR188866	Sequence
28	5	2.5	17	6	AR188867	Sequence
29	5	2.5	17	6	AR188868	Sequence
30	5	2.5	17	6	AR191815	Sequence
31	5	2.5	17	6	AR191816	Sequence
C 32	5	2.5	17	6	AR193560	Sequence
33	5	2.5	17	6	AR285974	Sequence
34	5	2.5	17	6	AR232153	Sequence
35	5	2.5	17	6	AR323154	Sequence
36	5	2.5	17	6	AR324719	Sequence
37	5	2.5	17	6	AR324720	Sequence
38	5	2.5	17	6	AR324721	Sequence
39	5	2.5	17	6	AR325710	Sequence
40	5	2.5	17	6	AR325711	Sequence
41	5	2.5	17	6	AR327446	Sequence
42	5	2.5	17	6	AR397964	Sequence
C 43	5	2.5	17	6	AX214940	Sequence
C 44	5	2.5	17	6	AX215777	Sequence
C 45	5	2.5	17	6	AX215821	Sequence

ALIGNMENTS

RESULT 1

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AR300029      LOCUS       18 bp      DNA
DEFINITION   Sequence 11764 from patent US 6537751.
ACCESSION   AR300029
VERSION     AR300029.1  GI:31687313
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
JOURNAL    Patent: US 6537751-A 11764 25-MAR-2003;
FEATURES    Location/Qualifiers
             1..18
             /organism="unknown"
             /mol_type="genomic DNA"
ORIGIN
Alignment Scores:      710      Length:      18
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches: 0
Best Local Similarity: 3.03%      Indels:      0
Query Match:           3.03%      Gaps:        0
DB:
US-09-966-880A-8 (1-198) x AR300029 (1-18)

QY      179  IleLeuLeuProLeuTyr 184
|||||
Db      1  ATCCTTCTCCACTCTAC 18

RESULT 2
AR295883/c
LOCUS       19 bp      DNA
DEFINITION   Sequence 7618 from patent US 6537751.
ACCESSION   AR295883
VERSION     AR295883.1  GI:31683167
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
JOURNAL    Patent: US 6537751-A 7618 25-MAR-2003;
FEATURES    Location/Qualifiers
             1..19
             /organism="unknown"
             /mol_type="genomic DNA"
ORIGIN
Alignment Scores:      744      Length:      19
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches: 0
Best Local Similarity: 3.03%      Indels:      0
Query Match:           3.03%      Gaps:        0
DB:
US-09-966-880A-8 (1-198) x AR295883 (1-19)

QY      167  GluAsnSerValArgLeu 172
|||||
Db      19  GAAATAGTGTAGGCTC 2

RESULT 3
AR026495
LOCUS       20 bp      DNA
DEFINITION   Sequence 2 from patent US 5856099.
ACCESSION   AR026495
VERSION
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Miraglia,L., Bennett,C.Frank., Dean,N. and Geiger,T.
TITLE      Antisense compositions and methods for modulating type I
JOURNAL    Patent: US 5856099-A 2 05-JAN-1999;
FEATURES    Location/Qualifiers
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:      778      Length:      20
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches: 0
Best Local Similarity: 3.03%      Indels:      0
Query Match:           3.03%      Gaps:        0
DB:
US-09-966-880A-8 (1-198) x AR026495 (1-20)

QY      125  GlyLeuArgArgLeuHis 130
|||||
Db      2  GGGCTGGCGCGCTCCAC 19

RESULT 4
AR224722/c
LOCUS       20 bp      DNA
DEFINITION   Sequence 27 from patent US 6440739.
ACCESSION   AR224722
VERSION     AR224722.1  GI:23333562
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Bennett,C.F. and Freier,S.M.
TITLE      Antisense modulation of glioma-associated oncogene-2 expression
JOURNAL    Patent: US 6440739-A 27 27-AUG-2002;
FEATURES    Location/Qualifiers
             1..20
             /organism="unknown"
             /mol_type="genomic DNA"
ORIGIN
Alignment Scores:      778      Length:      20
Pred. No.:             6.00      Matches:      6
Score:                 100.00%    Conservative: 0
Percent Similarity:    100.00%    Mismatches: 0
Best Local Similarity: 3.03%      Indels:      0
Query Match:           3.03%      Gaps:        0
DB:
US-09-966-880A-8 (1-198) x AR224722 (1-20)

QY      122  GluProGlyLeuArg 127
|||||
Db      18  GAGCCTGAGGCGCTGCGG 1

RESULT 5
AR297575
LOCUS       20 bp      DNA
DEFINITION   Sequence 9310 from patent US 6537751.
ACCESSION   AR297575
VERSION     AR297575.1  GI:31684859
KEYWORDS
SOURCE      Unknown.
```

```

ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE          Biallelic markers for use in constructing a high density
JOURNAL        disequilibrium map of the human genome
FEATURES       Patent: US 6537751-A 9310 25-MAR-2003;
               Location/Qualifiers
               1..20
               /organism="unknown"
ORIGIN         /mol_type="genomic DNA"
Alignment Scores:
Pred. No.:      778      Length:      20
Score:          6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    3.03%      Indels:      0
DB:             6         Gaps:        0

US-09-966-880A-8 (1-198) x AR297575 (1-20)

QY             40 ThrSerPheSerLeuAsp 45
Db             2 ACAGTTTCTCATTAGAC 19

RESULT 6
LOCUS          AR314839      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION     Sequence 5376 from patent US 6559294.
ACCESSION      AR314839
VERSION        AR314839.1 GI:31708265
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 5376 06-MAY-2003;
FEATURES       Location/Qualifiers
               1..20
               /organism="unknown"
ORIGIN         /mol_type="genomic DNA"
Alignment Scores:
Pred. No.:      778      Length:      20
Score:          6.00     Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    3.03%      Indels:      0
DB:             6         Gaps:        0

US-09-966-880A-8 (1-198) x AR314839 (1-20)

QY             167 GluAsnSerValArgLeu 172
Db             1 GAGAACTCGTGGCGCTG 18

RESULT 7
LOCUS          AR180659      15 bp      DNA      linear      PAT 20-APR-2002
DEFINITION     Sequence 727 from patent US 6333152.
ACCESSION      AR180659
VERSION        AR180659.1 GI:20222692
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)

AUTHORS        Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE          Gene expression profiles in normal and cancer cells
JOURNAL        Patent: US 6333152-A 727 25-DEC-2001;
FEATURES       Location/Qualifiers
               1..15
               /organism="unknown"
ORIGIN         /mol_type="unassigned DNA"
Alignment Scores:
Pred. No.:      7.11e+03  Length:      15
Score:          5.00     Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             6         Gaps:        0

US-09-966-880A-8 (1-198) x AR180659 (1-15)

QY             93 HisValAlaAspPhe 97
Db             1 CATGTTCTGACTTT 15

RESULT 8
LOCUS          AX322719/c    16 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION     Sequence 4 from Patent WO0192502.
ACCESSION      AX322719
VERSION        AX322719.1 GI:18093709
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1
AUTHORS        Svendsen,A., Glad,S.O., Fukuyama,S. and Matsui,T.
TITLE          Cutinase variants
JOURNAL        Patent: WO 0192502-A 4 06-DEC-2001;
FEATURES       Location/Qualifiers
               1..16
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
               /note="Dop2-R"
ORIGIN         /mol_type="Dop2-R"
Alignment Scores:
Pred. No.:      7.52e+03  Length:      16
Score:          5.00     Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             6         Gaps:        0

US-09-966-880A-8 (1-198) x AX322719 (1-16)

QY             70 LeuAspProGlyArg 74
Db             16 CTGATCCAGGCGGT 2

RESULT 9
LOCUS          A35587        17 bp      DNA      linear      PAT 02-DEC-1996
DEFINITION     Synthetic human IFN-alpha 2 gene oligo.
ACCESSION      A35587
VERSION        A35587.1 GI:1926969
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS        Camble,R. and Edge,M.D.
TITLE          Analogous interferon polypeptides, process for their preparation

```

and pharmaceutical compositions containing them
Patent: EP 0194006-A 32 10-SEP-1986;
IMPERIAL CHEMICAL INDUSTRIES PLC

JOURNAL

FEATURES

source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A35587 (1-17)

Qy 157 ArgThrPheLysAla 161

Db 2 AGACGTTTAAGGCG 16

RESULT 10

A45700/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
1. .17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A45700 (1-17)

Qy 104 LeuSerLeuArgIle 108

Db 15 CTTTCACTCGGAAT 1

RESULT 11

AR039735/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
1. .17
/organism="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 583 15-SEP-1998;
Location/Qualifiers

JOURNAL

FEATURES

source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR039735 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 17 GAAGGACTTAAAGG 3

RESULT 12

AR039737/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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JOURNAL

COMMENT

FEATURES

SOURCE

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/mol_type="unassigned DNA"					
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ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR057431 (1-17)					
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Qy	58 GluLeuLeuPheLeu 62				
Dd	1 GAACGTGCTTCCTC 15				
<hr/>					
RESULT 14					
AR057487	AR057487	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1691 from patent US 5837542.				
DEFINITION	Accession				
ACCESSION	AR057487				
VERSION	AR057487.1 GI:5983064				
KEYWORDS	Unknown.				
SOURCE	Organism				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.				
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes				
JOURNAL	Patent: US 5837542-A 1691 17-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..17				
/organism="unknown"					
/mol_type="unassigned DNA"					
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ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR057487 (1-17)					
<hr/>					
Qy	58 GluLeuLeuPheLeu 62				
Dd	1 GAACGTGCTTCCTC 15				
<hr/>					
RESULT 15					
AR057687	AR057687	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1891 from patent US 5837542.				
DEFINITION	Accession				
ACCESSION	AR057687				
VERSION	AR057687.1 GI:5983264				
KEYWORDS	Unknown.				
SOURCE	Organism				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.				
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes				
JOURNAL	Patent: US 5837542-A 1891 17-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..17				
/organism="unknown"					
/mol_type="unassigned DNA"					
<hr/>					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR057777 (1-17)					
<hr/>					
Qy	58 GluLeuLeuPheLeu 62				
Dd	1 GAACGTGCTTCCTC 15				
<hr/>					
RESULT 17					
AR057782	AR057782	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1986 from patent US 5837542.				
DEFINITION	Accession				
ACCESSION	AR057782				
VERSION	AR057782.1 GI:5983359				
KEYWORDS	Unknown.				
SOURCE	Organism				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.				
TITLE	Intercellular adhesion molecule-1 (ICAM-1) ribozymes				
JOURNAL	Patent: US 5837542-A 1986 17-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..17				
/organism="unknown"					
/mol_type="unassigned DNA"					
<hr/>					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR057777 (1-17)					
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Qy	58 GluLeuLeuPheLeu 62				
Dd	1 GAACGTGCTTCCTC 15				
<hr/>					
RESULT 17					
AR057782	AR057782	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1986 from				

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR057782 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 1 GAACTGCTCTTCCTC 15

RESULT 18

AR115189 LOCUS linear PAT 16-MAY-2001

DEFINITION Sequence 1635 from patent US 6132967.

ACCESSION AR115189

VERSION AR115189.1 GI:14095511

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of

intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1635 17-OCT-2000;

FEATURES Location/Qualifiers

1..17

source

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115189 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 1 GAACTGCTCTTCCTC 15

RESULT 19

AR115245 LOCUS linear PAT 16-MAY-2001

DEFINITION Sequence 1691 from patent US 6132967.

ACCESSION AR115245

VERSION AR115245.1 GI:14095567

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of

intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1691 17-OCT-2000;

FEATURES Location/Qualifiers

1..17

source

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115245 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 1 GAACTGCTCTTCCTC 15

RESULT 20

AR115445 LOCUS linear PAT 16-MAY-2001

DEFINITION Sequence 1891 from patent US 6132967.

ACCESSION AR115445

VERSION AR115445.1 GI:14095767

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of

intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1891 17-OCT-2000;

FEATURES Location/Qualifiers

1..17

source

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR115445 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 1 GAACTGCTCTTCCTC 15

RESULT 21

AR115535 LOCUS linear PAT 16-MAY-2001

DEFINITION Sequence 1981 from patent US 6132967.

ACCESSION AR115535

VERSION AR115535.1 GI:14095857

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of

intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1981 17-OCT-2000;

FEATURES Location/Qualifiers

1..17

source

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

FT	source	1..17	/organism='Homo sapiens (human)'
FEATURES	Location/Qualifiers		
source	1..17		
ORIGIN			
Alignment Scores:			
Pred. No.:	7.93e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0
US-09-966-880A-8 (1-198) x BD241216 (1-17)			
QY	169 SerValArgLeuSer 173		
DB	3 ACGTCCGGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION	Regulation of repressor genes using nucleic acid molecules.		
ACCESSION	BD256674		
VERSION	BD256674.1 GI:33066444		
KEYWORDS	JP 2002541795-A/4467		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.		
TITLE	Regulation of repressor genes using nucleic acid molecules		
JOURNAL	Patent: JP 2002541795-A 4467 10-DEC-2002;		
COMMENT	RIBOZYME PHARMACEUTICALS INC		
OS	Eukaryote		
PN	JP 2002541795-A/4467		
PD	10-DEC-2002		
PF	11-APR-2000 JP 2000611654		
PR	12-APR-1999 US 60/129390		
PI	LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC		
CI2N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,CI2N5/10, PC			
CI2P21/02,			
PC			
CI2P21/02,CI2P21/02//A61K31/711,(CI2N5/10,CI2R1/91),(CI2P21/02, PC			
CI2R1/91),			
PC	(CI2P21/02,CI2R1/91),(CI2P21/02,CI2R1/91),CI2N15/00,CI2N5/00,		
PC	A61K37/02,PC		
PC	(CI2N5/00,CI2R1/91)		
CC	Regulation of repressor genes using nucleic acid molecules FH		
Key	Location/Qualifiers		
FT	source		
1..17			
Location/Qualifiers			
/organism='Eukaryote'			
/organism='unidentified'			
/mol_type='genomic DNA'			
/db_xref='taxon:32644'			
ORIGIN			
Alignment Scores:			
Pred. No.:	7.93e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0
US-09-966-880A-8 (1-198) x BD256674 (1-17)			
QY	169 SerValArgLeuSer 173		
DB	3 ACGTCCGGTTAAGT 17		
RESULT 24			
BD256674/c			
LOCUS			
DEFINITION	Regulation of repressor genes using nucleic acid molecules		
ACCESSION	BD256674		
VERSION	BD256674.1 GI:33066444		
KEYWORDS	JP 2002541795-A/4467		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.		
TITLE	Regulation of repressor genes using nucleic acid molecules		
JOURNAL	Patent: JP 2002541795-A 4467 10-DEC-2002;		
COMMENT	RIBOZYME PHARMACEUTICALS INC		
OS	Eukaryote		
PN	JP 2002541795-A/4467		
PD	10-DEC-2002		
PF	11-APR-2000 JP 2000611654		
PR	12-APR-1999 US 60/129390		
PI	LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC		
CI2N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,CI2N5/10, PC			
CI2P21/02,			
PC			
CI2P21/02,CI2P21/02//A61K31/711,(CI2N5/10,CI2R1/91),(CI2P21/02, PC			
CI2R1/91),			
PC	(CI2P21/02,CI2R1/91),(CI2P21/02,CI2R1/91),CI2N15/00,CI2N5/00,		
PC	A61K37/02,PC		
PC	(CI2N5/00,CI2R1/91)		
CC	Regulation of repressor genes using nucleic acid molecules FH		
Key	Location/Qualifiers		
FT	source		
1..17			
Location/Qualifiers		</	

Qy	11 PhleuryGlnPhe 15 15 TTTCTCATCAGTTC 1
Db	
RESULT 25	AR186522
LOCUS	AR186522
DEFINITION	Sequence 2010 from patent US 6346398.
ACCESSION	AR186522
VERSION	AR186522.1 GI:20232487
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6346398-A 2010 12-FEB-2002;
FEATURES	source 1..17 Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	Pred. No.: Length: 17
Score:	7.93e+03 Matches: 5
Percent Similarity:	5.00 Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	2.53% Gaps: 0
US-09-966-880A-8 (1-198) x AR186522 (1-17)	
Qy	102 ProAsnLeuSerLeu 106 3 CCGAATCTATCTTG 17
Db	
RESULT 26	AR186523
LOCUS	AR186523
DEFINITION	Sequence 2011 from patent US 6346398.
ACCESSION	AR186523
VERSION	AR186523.1 GI:20232488
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6346398-A 2011 12-FEB-2002;
FEATURES	source 1..17 Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	Pred. No.: Length: 17
Score:	7.93e+03 Matches: 5
Percent Similarity:	5.00 Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	2.53% Gaps: 0
US-09-966-880A-8 (1-198) x AR186523 (1-17)	
Qy	102 ProAsnLeuSerLeu 106 1 CCGAATCTATCTTG 15
Db	

RESULT 27	AR188866
LOCUS	AR188866
DEFINITION	Sequence 4354 from patent US 6346398.
ACCESSION	AR188866
VERSION	AR188866.1 GI:20234831
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6346398-A 4354 12-FEB-2002;
FEATURES	source 1..17 Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	Pred. No.: Length: 17
Score:	7.93e+03 Matches: 5
Percent Similarity:	5.00 Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	2.53% Gaps: 0
US-09-966-880A-8 (1-198) x AR188866 (1-17)	
Qy	157 ArgThrPheLysAla 161 3 AGAACTTTTAAGCT 17
Db	
RESULT 28	AR188867
LOCUS	AR188867
DEFINITION	Sequence 4355 from patent US 6346398.
ACCESSION	AR188867
VERSION	AR188867.1 GI:20234832
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6346398-A 4355 12-FEB-2002;
FEATURES	source 1..17 Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	Pred. No.: Length: 17
Score:	7.93e+03 Matches: 5
Percent Similarity:	5.00 Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	2.53% Gaps: 0
US-09-966-880A-8 (1-198) x AR188867 (1-17)	
Qy	157 ArgThrPheLysAla 161 2 AGAACTTTTAAGCT 15
Db	
RESULT 29	AR188868
LOCUS	AR188868
DEFINITION	Sequence 4356 from patent US 6346398.
ACCESSION	AR188868
VERSION	AR188868.1 GI:20234833
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6346398-A 4356 12-FEB-2002;
FEATURES	source 1..17 Location/Qualifiers /organism="unknown" /mol_type="unassigned DNA"
ORIGIN	
Alignment Scores:	Pred. No.: Length: 17
Score:	7.93e+03 Matches: 5
Percent Similarity:	5.00 Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	2.53% Gaps: 0
US-09-966-880A-8 (1-198) x AR188868 (1-17)	
Qy	102 ProAsnLeuSerLeu 106 1 CCGAATCTATCTTG 15
Db	

LOCUS AR188868 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4356 from patent US 6346398.
ACCESSION AR188868
VERSION AR188868.1 GI:20234833
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4356 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 7.93e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR188868 (1-17)
QY 157 ArgThrPheLysAla 161
Db 1 AGAACTTTTAAAGCT 15
RESULT 30
AR191815
LOCUS AR191815 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7303 from patent US 6346398.
ACCESSION AR191815
VERSION AR191815.1 GI:20237780
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7303 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 7.93e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR191815 (1-17)
QY 179 IleLeuLeuProLeu 183
Db 2 ATACTCTTACCCCTG 16
RESULT 31
AR191816
LOCUS AR191816 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7304 from patent US 6346398.
ACCESSION AR191816

VERSION AR191816.1 GI:20237781
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7304 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 7.93e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR191816 (1-17)
QY 179 IleLeuLeuProLeu 183
Db 1 ATACTCTTACCCCTG 15
RESULT 32
AR193560/c
LOCUS AR193560 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 31 from patent US 6348313.
ACCESSION AR193560
VERSION AR193560.1 GI:20240152
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sibson,D.,Koss.
TITLE Sequencing of nucleic acids
JOURNAL Patent: US 6348313-A 31 19-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores: 7.93e+03 Length: 17
Pred. No.: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR193560 (1-17)
QY 104 LeuSerLeuArgIle 108
Db 15 CTTTCACTCCGAATT 1
RESULT 33
AR285974
LOCUS AR285974 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 346 from patent US 6528640.
ACCESSION AR285974
VERSION AR285974.1 GI:29723570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

FEATURES	source	Location/Qualifiers	1. .17	/organism="unknown"	/mol_type="unassigned RNA"
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR324720 (1-17)					
Qy	157 ArgThrPheLysAla 161				
Db	2 AGAACITTTAAAGCT 16				
RESULT 38					
AR324721					
LOCUS	AR324721	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 2123 from patent US 6566127.				
ACCESSION	AR324721				
VERSION	AR324721.1 GI:33710529				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 2123 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR324721 (1-17)					
Qy	157 ArgThrPheLysAla 161				
Db	1 AGAACITTTAAAGCT 15				
RESULT 39					
AR325710					
LOCUS	AR325710	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 3112 from patent US 6566127.				
ACCESSION	AR325710				
VERSION	AR325710.1 GI:33711518				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 3112 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR325711 (1-17)					
Qy	179 IleLeuLeuProLeu 183				
Db	1 ATACTCTTACCCCTG 15				
RESULT 41					
AR327446					
LOCUS	AR327446	17 bp RNA	linear	PAT 17-AUG-2003	
DEFINITION	Sequence 4848 from patent US 6566127.				
ACCESSION	AR327446				
VERSION	AR327446.1 GI:33713254				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 4848 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1. .17				
/organism="unknown"					
/mol_type="unassigned RNA"					
ORIGIN					
Alignment Scores:					
Pred. No.:	7.93e+03	Length:	17		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		

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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR327446 (1-17)

Qy 102 ProAsnLeuSerLeu 106
Db 2 CCGAATCTATCTTG 16

RESULT 42
LOCUS AR397964 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 345 from patent US 6617438.
ACCESSION AR397964
VERSION AR397964.1 GI:40135388
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 345 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR397964 (1-17)

Qy 89 AspCysAlaArgHis 93
Db 3 GATTGTGCGAGGCAC 17

RESULT 43
LOCUS AX214940/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 382 from Patent WO0159103.
ACCESSION AX214940
VERSION AX214940.1 GI:15524983
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 382 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215777 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 16 GAGCTTCTGTTCTT 2

RESULT 45
LOCUS AX215821/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1263 from Patent WO0159103.
ACCESSION AX215821
VERSION AX215821.1 GI:15525864
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1263 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX214940 (1-17)

Qy 169 SerValArgLeuSer 173
Db 16 TCAGTGAGACTTCT 2

RESULT 44
LOCUS AX215777/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1219 from Patent WO0159103.
ACCESSION AX215777
VERSION AX215777.1 GI:15525820
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1219 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215777 (1-17)

Qy 58 GluLeuLeuPheLeu 62
Db 16 GAGCTTCTGTTCTT 2

RESULT 45
LOCUS AX215821/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1263 from Patent WO0159103.
ACCESSION AX215821
VERSION AX215821.1 GI:15525864
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 1263 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"

ORIGIN

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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215931 (1-17)

Qy 169 SerValArgLeuSer 173
Db 15 TCAGTGAGACTTCT 1

RESULT 46

AX215931/c
LOCUS AX215931 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1373 from Patent WO0159103.
ACCESSION AX215931
VERSION AX215931.1 GI:15525974

KEYWORDS
SOURCE
ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Blatt, L., Meswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression

JOURNAL

Patent: WO 0159103-A 1373 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES

source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215931 (1-17)

Qy 194 ArgThrLeuGlyLeu 198
Db 17 AGAAGTTGGGTTTA 3

RESULT 47

AX215932/c
LOCUS AX215932 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1374 from Patent WO0159103.
ACCESSION AX215932
VERSION AX215932.1 GI:15525975

KEYWORDS
SOURCE
ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Blatt, L., Meswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression

JOURNAL Patent: WO 0159103-A 1374 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES

source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX215932 (1-17)

Qy 194 ArgThrLeuGlyLeu 198
Db 16 AGAAGTTGGGTTTA 2

RESULT 48

AX216798
LOCUS AX216798 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2240 from Patent WO0159103.
ACCESSION AX216798
VERSION AX216798.1 GI:15526859

KEYWORDS
SOURCE
ORGANISM

synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Blatt, L., Meswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression

JOURNAL

Patent: WO 0159103-A 2240 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES

source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX216798 (1-17)

Qy 8 ArgArgLysPheLeu 12
Db 1 AGGAGAAATTCCTT 15

RESULT 49

AX217113/c
LOCUS AX217113 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2555 from Patent WO0159103.
ACCESSION AX217113
VERSION AX217113.1 GI:15527174

KEYWORDS
SOURCE
ORGANISM

synthetic construct
synthetic construct

artificial sequences.

```

REFERENCE
1
AUTHORS
Blatt,L., Mcswiggen,J. and Chowrira,B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2555 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX217113 (1-17)
QY 58 GluleuLeuPheLeu 62
Db |||||
15 GAGCTTCGTGTTCTT 1
RESULT 50
AX264024 17 bp DNA linear PAT 26-OCT-2001
LOCUS
AX264024
DEFINITION
Sequence 1415 from Patent WO0173002.
ACCESSION
AX264024
VERSION
AX264024.1 GI:16512823
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 1415 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
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Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX264024 (1-17)
QY 129 LeuHisArgAlaGly 133
Db |||||
2 CTGCACCGGCGCGG 16
RESULT 51
AX264025/c
LOCUS
AX264025
DEFINITION
Sequence 1416 from Patent WO0173002.
ACCESSION
AX264025

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VERSION
AX264025.1 GI:16512824
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 1416 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX264025 (1-17)
QY 129 LeuHisArgAlaGly 133
Db |||||
16 CTGCACCGGCGCGG 2
RESULT 52
AX2666427/c
LOCUS
AX2666427
DEFINITION
Sequence 3818 from Patent WO0173002.
ACCESSION
AX2666427
VERSION
AX2666427.1 GI:16515226
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL
Patent: WO 0173002-A 3818 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX2666427 (1-17)
QY 93 HisValAlaAspPhe 97
Db |||||
15 CATGTTGAGACTTT 1
RESULT 53
AX2666428

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LOCUS       AX266428                      17 bp      DNA
DEFINITION   Sequence 3819 from Patent WO0173002.
ACCESSION    AX266428
VERSION      AX266428.1  GI:16515227
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
              stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 3819 04-OCT-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:       0
US-09-966-880A-8 (1-198) x AX266428 (1-17)

QY          93 HisValAlaAspPhe 97
DB          3 CATGTTGCAGACTTT 17

RESULT 54
AX280085
LOCUS       AX280085                      17 bp      DNA
DEFINITION   Sequence 14 from Patent WO0177295.
ACCESSION    AX280085
VERSION      AX280085.1  GI:16607527
KEYWORDS     Aspergillus fumigatus
SOURCE       Aspergillus fumigatus
ORGANISM     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
              Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE    1
AUTHORS      Denning,D.W., Brookman,J.L., Rickers,A. and Birch,M.
TITLE        Mutant bank
JOURNAL      Patent: WO 0177295-A 14 18-OCT-2001;
              F2G Limited (GB)
FEATURES     source
              1..17
              /organism="Aspergillus fumigatus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:5085"
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Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:       0
US-09-966-880A-8 (1-198) x AX280085 (1-17)

QY          176 LeuAtcArgIleIeu 180
DB          3 TTGAGCGCAATTC TC 17

LOCUS       AX324869/c                    17 bp      DNA
DEFINITION   Sequence 1007 from Patent WO0192512.
ACCESSION    AX324869
VERSION      AX324869.1  GI:18095623
KEYWORDS     Arabidopsis thaliana (thale cress)
SOURCE       Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE        Targeted chromosomal genomic alterations in plants using modified
              single stranded oligonucleotides
JOURNAL      Patent: WO 0192512-A 1007 06-DEC-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Arabidopsis thaliana"
              /mol_type="unassigned DNA"
              /db_xref="taxon:3702"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:       0
US-09-966-880A-8 (1-198) x AX324869 (1-17)

QY          32 ValVallyeArgArg 36
DB          15 GTTGTCAAGAGAGA 1

RESULT 56
AX324870
LOCUS       AX324870                      17 bp      DNA
DEFINITION   Sequence 1008 from Patent WO0192512.
ACCESSION    AX324870
VERSION      AX324870.1  GI:18095624
KEYWORDS     Arabidopsis thaliana (thale cress)
SOURCE       Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE    1
AUTHORS      Kniec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE        Targeted chromosomal genomic alterations in plants using modified
              single stranded oligonucleotides
JOURNAL      Patent: WO 0192512-A 1008 06-DEC-2001;
              UNIVERSITY OF DELAWARE (US)
FEATURES     source
              1..17
              /organism="Arabidopsis thaliana"
              /mol_type="unassigned DNA"
              /db_xref="taxon:3702"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:       0
US-09-966-880A-8 (1-198) x AX324870 (1-17)

QY          176 LeuAtcArgIleIeu 180
DB          3 TTGAGCGCAATTC TC 17

```



```

QY      32 ValValLysArgArg 36
DB      |||||
        3 GTTGTCARAAGGAGA 17

RESULT 57
LOCUS   AX325133              17 bp      DNA
DEFINITION
Sequence 1271 from Patent WO0192512.
ACCESSION
AX325133
VERSION
AX325133.1 GI:18095888
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1271 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 58
LOCUS   AX325134/C           17 bp      DNA
DEFINITION
Sequence 1272 from Patent WO0192512.
ACCESSION
AX325134
VERSION
AX325134.1 GI:18095889
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1272 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
source
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/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 59
LOCUS   AX499899              17 bp      DNA
DEFINITION
Sequence 1206 from Patent EP1229046.
ACCESSION
AX499899
VERSION
AX499899.1 GI:23382192
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1206 07-AUG-2002;
Acomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      172 LeuSerArgGlnLeu 176
DB      |||||
        3 CTTTCCAGCACTG 17

RESULT 60
LOCUS   AX499900              17 bp      DNA
DEFINITION
Sequence 1207 from Patent EP1229046.
ACCESSION
AX499900
VERSION
AX499900.1 GI:23382193
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1207 07-AUG-2002;
Acomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 61
LOCUS   AX325133              17 bp      DNA
DEFINITION
Sequence 1271 from Patent WO0192512.
ACCESSION
AX325133
VERSION
AX325133.1 GI:18095888
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1271 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
source
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/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 62
LOCUS   AX325134/C           17 bp      DNA
DEFINITION
Sequence 1272 from Patent WO0192512.
ACCESSION
AX325134
VERSION
AX325134.1 GI:18095889
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1
AUTHORS
Knies, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE
Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL
Patent: WO 0192512-A 1272 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Triticum aestivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325133 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 63
LOCUS   AX499899              17 bp      DNA
DEFINITION
Sequence 1206 from Patent EP1229046.
ACCESSION
AX499899
VERSION
AX499899.1 GI:23382192
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1206 07-AUG-2002;
Acomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      172 LeuSerArgGlnLeu 176
DB      |||||
        3 CTTTCCAGCACTG 17

RESULT 64
LOCUS   AX499900              17 bp      DNA
DEFINITION
Sequence 1207 from Patent EP1229046.
ACCESSION
AX499900
VERSION
AX499900.1 GI:23382193
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1207 07-AUG-2002;
Acomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX499899 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        3 CGACTGAGTCGTCAG 17

RESULT 65
LOCUS   AX325133              17 bp      DNA
DEFINITION
Sequence 1271 from Patent WO0192512.
ACCESSION
AX325133
VERSION
AX325133.1 GI:18095888
KEYWORDS
Triticum aestivum (bread wheat)
SOURCE
Triticum aestivum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheostomi;
Spermatophyta; Magnoliophyta; Liliopsida; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Zhan, J.
TITLE
Human testis expressed patched like protein
JOURNAL
Patent: EP 1229046-A 1207 07-AUG-2002;
Acomica, Inc. (US)
FEATURES
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX325134 (1-17)

QY      171 ArgLeuSerArgGln 175
DB      |||||
        15 CGACTGAGTCGTCAG 1

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Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 6
 Gaps: 0

Score: 5.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AX499900 (1-17)

QY 172 LeuSerArgGlnLeu 176
 DB 2 CTTTCAGCACTG 16

RESULT 61
 AX499901
 LOCUS AX499901 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 1208 from Patent EP1229046.
 ACCESSION AX499901
 VERSION AX499901.1 GI:23382194
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

RESULT 63
 AX531952
 LOCUS AX531952 17 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 1461 from Patent EP1239051.
 ACCESSION AX531952
 VERSION AX531952.1 GI:25255673
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Zhan, J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 1208 07-AUG-2002;
 Acomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

REFERENCE 1
 AUTHORS Shannon, M.
 TITLE Human posh-like protein 1
 JOURNAL Patent: EP 1239051-A 1461 11-SEP-2002;
 Acomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 7.93e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 6
 Gaps: 0

ORIGIN

Alignment Scores:
 Pred. No.: 7.93e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AX499901 (1-17)

QY 172 LeuSerArgGlnLeu 176
 DB 1 CTTTCAGCACTG 15

RESULT 62
 AX531951
 LOCUS AX531951 17 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 1460 from Patent EP1239051.
 ACCESSION AX531951
 VERSION AX531951.1 GI:25255672
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

RESULT 64
 AX531953
 LOCUS AX531953 17 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 1462 from Patent EP1239051.
 ACCESSION AX531953
 VERSION AX531953.1 GI:25255675
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

REFERENCE 1
 AUTHORS Shannon, M.
 TITLE Human posh-like protein 1
 JOURNAL Patent: EP 1239051-A 1460 11-SEP-2002;
 Acomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

REFERENCE 1
 AUTHORS Shannon, M.
 TITLE Human posh-like protein 1
 JOURNAL Patent: EP 1239051-A 1461 11-SEP-2002;
 Acomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 7.93e+03 Length: 17

ORIGIN

Alignment Scores:

Pred. No.: 17 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX531953 (1-17)

QY 21 AlalysglvArg 25
Db 1 GCAAAAGGAGAGG 15

RESULT 65
AX578371/c
LOCUS AX578371 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 209 from Patent WO0211674.
ACCESSION AX578371
VERSION AX578371.1 GI:27647573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 209 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX578371 (1-17)

QY 126 LeuArgLeuHis 130
Db 16 CTCGAGATTGCAT 2

RESULT 66
AX578929/c
LOCUS AX578929 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 767 from Patent WO0211674.
ACCESSION AX578929
VERSION AX578929.1 GI:27648131
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 767 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
Location/Qualifiers

source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX578929 (1-17)

QY 126 LeuArgLeuHis 130
Db 15 CTCGAGATTGCAT 1

RESULT 67
AX579988/c
LOCUS AX579988 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1826 from Patent WO0211674.
ACCESSION AX579988
VERSION AX579988.1 GI:27649190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1826 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 17 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX579988 (1-17)

QY 103 AsnLeuSerLeuArg 107
Db 15 AACTTGCTCTGAGA 1

RESULT 68
AX580320/c
LOCUS AX580320 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2158 from Patent WO0211674.
ACCESSION AX580320
VERSION AX580320.1 GI:27649522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.

and Grupe, A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (Clca-1)
Patent: WO 0211674-A 2159 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX580320 (1-17)

QY 103 AsnLeuSerLeuArg 107
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Db 16 AACTGCTCTGAGA 2

RESULT 69
AX634492
LOCUS AX634492 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1631 from Patent EP1260586.
ACCESSION AX634492
VERSION AX634492.1 GI:28470106
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
genes

TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1631 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
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/organism="unidentified"
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/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634492 (1-17)

QY 58 GluLeuLeuPheLeu 62
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Db 1 GAACGCTCTTCCTC 15

RESULT 70
AX634523
LOCUS AX634523 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1662 from Patent EP1260586.
ACCESSION AX634523

VERSION AX634523.1 GI:28470137
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
genes

TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1662 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
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/mol_type="unassigned RNA"
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ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634523 (1-17)

QY 58 GluLeuLeuPheLeu 62
|||||
Db 1 GAACGCTCTTCCTC 15

RESULT 71
AX634727
LOCUS AX634727 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1866 from Patent EP1260586.
ACCESSION AX634727
VERSION AX634727.1 GI:28470341
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
Method and reagent for inhibiting the expression of disease related
genes

TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1866 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634727 (1-17)

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Qy 58 GluleuLeuPheLeu 62
Db 1 GAACTGCTCTCTCCTC 15

RESULT 72
AX634809
LOCUS AX634809 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1948 from Patent EP1260586.
ACCESSION AX634809
VERSION AX634809.1 GI:28470423
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1948 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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source 1. .17
Location/Qualifiers
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Pred. No.: 7.93e+03 Length: 17
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634809 (1-17)

Qy 58 GluleuLeuPheLeu 62
Db 1 GAACTGCTCTCTCCTC 15

RESULT 73
AX634819
LOCUS AX634819 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1958 from Patent EP1260586.
ACCESSION AX634819
VERSION AX634819.1 GI:28470433
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1958 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1. .17
Location/Qualifiers
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Pred. No.: 7.93e+03 Length: 17
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX634809 (1-17)

Qy 58 GluleuLeuPheLeu 62
Db 1 GAACTGCTCTCTCCTC 15

RESULT 74
AX671739
LOCUS AX671739 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 184 from Patent WO03004526.
ACCESSION AX671739
VERSION AX671739.1 GI:29330087
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 184 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX671739 (1-17)

Qy 173 SerArgGlnLeuArg 177
Db 3 TCAAGGCAGCTGAGA 17

RESULT 75
AX673136
LOCUS AX673136 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1581 from Patent WO03004526.
ACCESSION AX673136
VERSION AX673136.1 GI:29331484
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1581 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1. .17
Location/Qualifiers
/organism="Homo sapiens"

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/moi_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX673136 (1-17)

Qy 43 SerLeuAspGly 47
Db 3 TCCCTGGACTTTGGA 17

RESULT 76
AX673244
LOCUS AX673244 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1689 from Patent WO03004526.
ACCESSION AX673244
VERSION AX673244.1 GI:29331592
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1689 16-JAN-2003;
FEATURES
source Molecular Engines Laboratories (FR)
location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX673244 (1-17)

Qy 169 SerValArgLeuSer 173
Db 3 TCCGTCGCGCTCAGC 17

RESULT 77
AX673640
LOCUS AX673640 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2085 from Patent WO03004526.
ACCESSION AX673640
VERSION AX673640.1 GI:29331988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1689 16-JAN-2003;
FEATURES
source Molecular Engines Laboratories (FR)
location/Qualifiers
1. .17
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/mol_type="unassigned DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX673397 (1-17)

Qy 59 LeuLeuPheLeuArg 63
Db 17 CTTCCTGTTTGTGAGA 3

RESULT 79
AX674498
LOCUS AX674498 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2943 from Patent WO03004526.
ACCESSION AX674498
VERSION AX674498.1 GI:29332846
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

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JOURNAL Patent: WO 03004526-A 2085 16-JAN-2003;
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source Molecular Engines Laboratories (FR)
location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX673640 (1-17)

Qy 118 AspArgGlySalGlu 122
Db 1 GATCGCAGGCTGAG 15

RESULT 78
AX673997/c
LOCUS AX673997 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2442 from Patent WO03004526.
ACCESSION AX673997
VERSION AX673997.1 GI:29332345
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2442 16-JAN-2003;
FEATURES
source Molecular Engines Laboratories (FR)
location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX673997 (1-17)

Qy 59 LeuLeuPheLeuArg 63
Db 17 CTTCCTGTTTGTGAGA 3

RESULT 79
AX674498
LOCUS AX674498 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2943 from Patent WO03004526.
ACCESSION AX674498
VERSION AX674498.1 GI:29332846
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or resistance to viruses and their use as
  medicines
JOURNAL
  Patent: WO 03004526-A 2943 16-JAN-2003;
  Molecular Engines Laboratories (FR)
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QY 169 SerValargLeuSer 173
Db 3 TCTGTCGCGCTCAGC 17
RESULT 80
AX723243
LOCUS AX723243 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 930 from Patent WO03025176.
ACCESSION AX723243
VERSION AX723243.1 GI:30423744
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
  medicines
JOURNAL
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Db 1 GATCCGGCAGGTGT 15
RESULT 81
AX723989
LOCUS AX723989 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1676 from Patent WO03025176.
ACCESSION AX723989
VERSION AX723989.1 GI:30503332

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KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
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JOURNAL
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  Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
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QY 179 IleLeuLeuProLeu 183
Db 2 ATCCTCTGCCACTG 16
RESULT 82
AX724877
LOCUS AX724877 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2564 from Patent WO03025176.
ACCESSION AX724877
VERSION AX724877.1 GI:30504220
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in phenomena of tumour suppression, tumour
  reversion, apoptosis and/or virus resistance and their use as
  medicines
JOURNAL
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  Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
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Db 3 TCCCTGGACTTTGCT 17
RESULT 83

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DEFINITION Sequence 4421 from Patent WO03025176.
ACCESSION AX726734
VERSION AX726734.1 GI:30506077
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
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medicines
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Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
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2 ATCCTCTTCTCTCTG 16
Db
RESULT 84
AX727644
LOCUS AX727644 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5331 from Patent WO03025176.
ACCESSION AX727644
VERSION AX727644.1 GI:30506987
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
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Molecular Engines Laboratories (FR)
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Score: 5.00 Matches: 5
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AX727644 (1-17)
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Db
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ACCESSION AX727644
VERSION AX727644.1 GI:30506987
KEYWORDS
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ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
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JOURNAL Patent: WO 03025176-A 5331 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AX727644 (1-17)
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Qy
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2 ATCCTCTTCTCTCTG 16
Db
RESULT 85
AX727871
LOCUS AX727871 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5558 from Patent WO03025176.
ACCESSION AX727871
VERSION AX727871.1 GI:30507214
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5558 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match: 2.53% Indels: 0
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US-09-966-880A-8 (1-198) x AX727871 (1-17)
Qy
179 IleleuLeuProleu 183
|||||
2 ATCCTCTTCTCTCTG 16
Db
RESULT 86
AX728573
LOCUS AX728573 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 207 from Patent WO03025175.
ACCESSION AX728573
VERSION AX728573.1 GI:30507916
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
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JOURNAL Patent: WO 03025175-A 207 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match:      2.53%      Indels:      0
DB:               6          Gaps:         0

US-09-966-880A-8 (1-198) x AX728573 (1-17)

Qy  83 SerTspSerProCys 87
Db   3 TCCTGGAGCCCTGT 17

RESULT 87
LOCUS AX730844/c          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2478 from Patent WO03025175.
ACCESSION AX730844
VERSION AX730844.1 GI:30510187
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2478 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    2.53%          Indels:      0
DB:             6            Gaps:         0

US-09-966-880A-8 (1-198) x AX730844 (1-17)

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Db   15 GCTGGAGTGCAGATC 1

RESULT 88
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DEFINITION Sequence 3542 from Patent WO03025175.
ACCESSION AX731908
VERSION AX731908.1 GI:30511251
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 3542 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    2.53%          Indels:      0
DB:             6            Gaps:         0

US-09-966-880A-8 (1-198) x AX731908 (1-17)

Qy  43 SerLeuAspPheGly 47
Db   3 TCCTAGATTTCGGT 17

RESULT 90
LOCUS AX735306          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 896 from Patent WO03025177.
ACCESSION AX735306
VERSION AX735306.1 GI:30514583
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 896 27-MAR-2003;
Molecular Engines Laboratories (FR)
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DB:             6            Gaps:         0

US-09-966-880A-8 (1-198) x AX735213 (1-17)

Qy  118 AspArgLysAlaGlu 122
Db   1 GATCGCAAGGCTGAG 15

RESULT 89
LOCUS AX735213          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 803 from Patent WO03025177.
ACCESSION AX735213
VERSION AX735213.1 GI:30514490
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 803 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Pred. No.:      7.93e+03      Length:      17
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Query Match:    2.53%          Indels:      0
DB:             6            Gaps:         0

US-09-966-880A-8 (1-198) x AX731908 (1-17)

Qy  118 AspArgLysAlaGlu 122
Db   1 GATCGCAAGGCTGAG 15

RESULT 89
LOCUS AX735213          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 803 from Patent WO03025177.
ACCESSION AX735213
VERSION AX735213.1 GI:30514490
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
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JOURNAL Patent: WO 03025177-A 803 27-MAR-2003;
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Best Local Similarity: 100.00%      Mismatches:  0
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US-09-966-880A-8 (1-198) x AX735213 (1-17)

Qy  43 SerLeuAspPheGly 47
Db   3 TCCTAGATTTCGGT 17

RESULT 90
LOCUS AX735306          17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 896 from Patent WO03025177.
ACCESSION AX735306
VERSION AX735306.1 GI:30514583
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 896 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match:	2.53%	Indels:
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Qy	59 LeuLeupheLeuArg 63	
Dd		
	CTTCTTTTCTGAGA 3	
RESULT 93		
LOCUS	AX739569	17 bp DNA
DEFINITION	Sequence 5159 from Patent WO03025177.	
ACCESSION	AX739569	
VERSION	AX739569.1 GI:30518866	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata	
	Mammalia; Euthera; Primates; Catarrhini	
REFERENCE		
AUTHORS	Teleman,A., Anson,R. and Tuijnder,M.	
TITLE	Sequences involved in phenomena of tumo-	
	reversion, apoptosis and/or resistance	
	thereof as medicaments	
JOURNAL	Patent: WO 03025177-A 5159 27-MAR-2003	
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US-09-966-880A-8 (1-198) x AX739569 (1-17)		
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Dd		
	GATCGCAAGCTTGAG 15	
RESULT 94		
LOCUS	AX756969/c	17 bp DNA
DEFINITION	Sequence 290 from Patent WO03040369.	
ACCESSION	AX756969	
VERSION	AX756969.1 GI:32251523	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata	

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REFERENCE
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AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
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JOURNAL
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Query Match: 2.53% Indels: 0
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Qy 46 PheGlyTyrLeuArg 50
Db 17 TTGGATATCTCAGA 3
RESULT 95
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ACCESSION
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VERSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
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  apoptosis and/or viral resistance phenomena and their use as
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Db 2 ATCTCTCTGCTCTG 16
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 3518 15-MAY-2003;
FEATURES
  Molecular Engines Laboratories (FR)
  source
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX760197 (1-17)
Qy 118 AspArgLysAlaGlu 122
Db 1 GATCGCAAGGCTGAG 15
RESULT 97
AX760666
LOCUS
  AX760666
DEFINITION
  Sequence 3987 from Patent WO03040369.
ACCESSION
  AX760666
VERSION
  AX760666.1 GI:32255282
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
ORGANISM
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
  Telerman,A., Anson,R. and Tuijnder,M.
TITLE
  Sequences involved in tumoral suppression, tumoral reversion,
  apoptosis and/or viral resistance phenomena and their use as
  medicines
JOURNAL
  Patent: WO 03040369-A 3987 15-MAY-2003;
FEATURES
  Molecular Engines Laboratories (FR)
  source
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AX760666 (1-17)
Qy 179 IleLeuLeuProLeu 183
Db 2 ATCTGTGTCATTG 16

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```

RESULT 98
AX762288      AX762288      17 bp      DNA      linear      PAT 25-JUN-2003
LOCUS         Sequence 5609 from Patent WO03040369.
DEFINITION    AX762288
ACCESSION     AX762288
VERSION       AX762288.1 GI:32256904
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS       Telerman,A., Anson,R. and Tuijinder,M.
TITLE         Sequences involved in tumoral suppression, tumoral reversion,
              apoptosis and/or viral resistance phenomena and their use as
              medicines
JOURNAL       Molecular Engines Laboratories (FR)
FEATURES      source
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0
US-09-966-880A-8 (1-198) x AX762288 (1-17)

QY           118 ASPARGLYNALAGLU 122
Db           1 GATCGCAAGCGCTGAG 15

RESULT 99
AX762491      AX762491      17 bp      DNA      linear      PAT 25-JUN-2003
LOCUS         Sequence 5812 from Patent WO03040369.
DEFINITION    AX762491
ACCESSION     AX762491
VERSION       AX762491.1 GI:32257107
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS       Telerman,A., Anson,R. and Tuijinder,M.
TITLE         Sequences involved in tumoral suppression, tumoral reversion,
              apoptosis and/or viral resistance phenomena and their use as
              medicines
JOURNAL       Molecular Engines Laboratories (FR)
FEATURES      source
              1. .17
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0
US-09-966-880A-8 (1-198) x AX762491 (1-17)

QY           43 SerLeuLapPheGly 47
Db           3 TCCTTAGATTGGG 17

RESULT 100
AX781934      AX781934      17 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Sequence 265 from Patent WO03050284.
DEFINITION    AX781934
ACCESSION     AX781934
VERSION       AX781934.1 GI:32949768
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS       Guo,J.
TITLE         Human prostate cancer candidate protein 1
JOURNAL       Patent: WO 03050284-A 265 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES      source
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0
US-09-966-880A-8 (1-198) x AX781934 (1-17)

QY           3 SerLeuLeuMetAen 7
Db           3 AGTTATTGATGAAT 17

RESULT 101
AX781935      AX781935      17 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Sequence 266 from Patent WO03050284.
DEFINITION    AX781935
ACCESSION     AX781935
VERSION       AX781935.1 GI:32949769
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS       Guo,J.
TITLE         Human prostate cancer candidate protein 1
JOURNAL       Patent: WO 03050284-A 266 19-JUN-2003;
              Amersham Biosciences (SV) Corp. (US)
FEATURES      source
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      7.93e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:              6           Gaps:          0
US-09-966-880A-8 (1-198) x AX781935 (1-17)

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US-09-966-880A-8 (1-198) x AX781935 (1-17)

Qy 3 SerLeuLeuMetAsn 7
|||||
Db 2 AGTTATTGATGAAT 16

RESULT 102

AX781936 AX781936 17 bp DNA linear PAT 17-JUL-2003
LOCUS Sequence 267 from Patent WO03050284.
ACCESSION AX781936
VERSION AX781936.1 GI:32949770
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Guo, J.
AUTHORS Human prostate cancer candidate protein 1
TITLE Patent: WO 03050284-A 267 19-JUN-2003;
JOURNAL Amersham Biosciences (SV) Corp. (US)

FEATURES

source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 17
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX781936 (1-17)

Qy 3 SerLeuLeuMetAsn 7
|||||
Db 1 AGTTATTGATGAAT 15

RESULT 103

BD105002/c BD105002 17 bp DNA linear PAT 27-AUG-2002
LOCUS Kit and method for determining HLA type.
DEFINITION
ACCESSION BD105002
VERSION BD105002.1 GI:22650576
KEYWORDS WO 0192572-A/1106.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 (bases 1 to 17)
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1106 06-DEC-2001;
NISHINO INDUSTRIES INC. SYSTEM RESEARCH INC. HIDEOTOSHI INOKO, TAEKO
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA

COMMENT

OS Artificial Sequence
PN WO 0192572-A/1106
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
MATSUMURA,
SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..17

FT Location/Qualifiers /organism='Artificial Sequence'

source 1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores: 17
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD105002 (1-17)

Qy 112 ArgLeuTyrPheCys 116

|||||
Db 15 CGCTTGACTTCTGT 1

RESULT 104

BD200916 BD200916 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD200916
VERSION BD200916.1 GI:33010686
KEYWORDS JP 2002509721-A/3942.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
COMMENT Patent: JP 2002509721-A 3942 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/3942
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00, A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
FH Key Location/Qualifiers
FT source 1..17
/organism="Homo sapiens (human)"

FEATURES

source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores: 17
Pred. No.: 7.93e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD200916 (1-17)

Qy 177 ArgArgIleLeu 181
Db 1 AGAAGGATATGCTT 15

RESULT 105

LOCUS A06176 18 bp DNA linear PAT 04-JUN-1993
DEFINITION Oligonucleotide probe (reverse complement).
ACCESSION A06176
VERSION A06176.1 GI:411212
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE GENE MODIFICATION
JOURNAL Patent: WO 9001549-A 4 22-FEB-1990;
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A06176 (1-18)

Qy 35 ArgArgAspSerAla 39
Db 17 CGCCGTCAGCTCAGCA 3

RESULT 106

LOCUS A40057 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 18 from Patent WO9421818.
ACCESSION A40057
VERSION A40057.1 GI:2296222
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Andrien.M., Dupont,E., Rossau,R. and De,C.I.
TITLE PROCESS FOR TYPING HLA-B USING SPECIFIC PRIMERS AND PROBES SETS
JOURNAL INNOCENTICS NV (BE)
COMMENT Other publication CA 2158578 940929
Other publication AU 6258594 941011.
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A40057 (1-18)

Qy 112 ArgLeuTyrPheCys 116
Db 17 CGCTTGACTTCTGT 3

RESULT 107

LOCUS AR016419 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776725.
ACCESSION AR016419
VERSION AR016419.1 GI:3972696
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kindsvogel,W.R., Jelinek,L.J., Sheppard,P.O., Grant,F.J.,
Kuijper,J.L., Foster,D.C., Lok,S. and O'Hara,P.J.
TITLE Recombinant production of glucagon receptors
JOURNAL Patent: US 5776725-A 2 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR016419 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACACGCG 16

RESULT 108

LOCUS AR072241 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 44 from patent US 5948611.
ACCESSION AR072241
VERSION AR072241.1 GI:99999005
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvanemi,P.,
Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
TITLE Primers and methods for detecting mutations in the procollagen II
gene (COL2A1) that indicate a genetic predisposition for a
COL2AL-associated disease
JOURNAL Patent: US 5948611-A 44 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..18
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/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR072241 (1-18)

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QY 69 AspLeuAspProGly 73
Db 3 GATCTGGATCCTGGA 17

RESULT 109
LOCUS AR073074/c 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 47 from patent US 5948680..
ACCESSION AR073074
VERSION AR073074.1 GI:9999837
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowseert,L.M.
TITLE Antisense inhibition of Elk-1 expression
JOURNAL Patent: US 5948680-A 47 07-SEP-1999;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR073074 (1-18)

QY 103 AsnLeuSerLeuArg 107
Db 17 AACCTTTCTCTCAGA 3

RESULT 110
LOCUS AR076296 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 10 from patent US 5958771.
ACCESSION AR076296
VERSION AR076296.1 GI:10003042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowseert,L.M.
TITLE Antisense modulation of cellular inhibitor of Apoptosis-2
expression
JOURNAL Patent: US 5958771-A 10 28-SEP-1999;
FEATURES
    Location/Qualifiers
        source
            1..18
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                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR076296 (1-18)

QY 59 LeuLeuPheLeuArg 63
Db 4 CTTTATTCTTCTAGA 18

RESULT 111
LOCUS AR076328 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 42 from patent US 5958771.
ACCESSION AR076328
VERSION AR076328.1 GI:10003074
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowseert,L.M.
TITLE Antisense modulation of cellular inhibitor of Apoptosis-2
expression
JOURNAL Patent: US 5958771-A 42 28-SEP-1999;
FEATURES
    Location/Qualifiers
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            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR076328 (1-18)

QY 38 SerAlaThrSerPhe 42
Db 4 AGTCTACCTCTTTT 18

RESULT 112
LOCUS AR094003 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 19 from patent US 6001597.
ACCESSION AR094003
VERSION AR094003.1 GI:10020748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K. and Vanaja,E.
TITLE Compositions and methods for producing heterologous polypeptides in
Pichia methanolica
JOURNAL Patent: US 6001597-A 19 14-DEC-1999;
FEATURES
    Location/Qualifiers
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            1..18
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                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR094003 (1-18)

QY 32 ValValIysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 113
LOCUS AR096629 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 19 from patent US 6001597.
ACCESSION AR096629
VERSION AR096629.1 GI:10020748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K. and Vanaja,E.
TITLE Compositions and methods for producing heterologous polypeptides in
Pichia methanolica
JOURNAL Patent: US 6001597-A 19 14-DEC-1999;
FEATURES
    Location/Qualifiers
        source
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR096629 (1-18)

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LOCUS       AR096629               18 bp      DNA
DEFINITION   Sequence 13 from patent US 6008048.
ACCESSION    AR096629
VERSION      AR096629.1  GI:10025595
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Monia,B.P. and Cowsest,L.M.
TITLE        Antisense inhibition of EGR-1 expression
JOURNAL      Patent: US 6008048-A 13 28-DEC-1999;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0
US-09-966-880A-8 (1-198) x AR096629 (1-18)
QY           127 ArgArgLeuHisArg 131
Db           4 CGCGCGCTCCACGC 18
RESULT 114
LOCUS       AR098797/c             18 bp      DNA
DEFINITION   Sequence 52 from patent US 6077672.
ACCESSION    AR098797
VERSION      AR098797.1  GI:12808563
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Monia,B.P. and Cowsest,L.M.
TITLE        Antisense modulation of TRADD expression
JOURNAL      Patent: US 6077672-A 52 20-JUN-2000;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0
US-09-966-880A-8 (1-198) x AR098797 (1-18)
QY           121 AlaGluProGluGly 125
Db           16 GCTGAGCCTGAAGGA 2
RESULT 115
LOCUS       AR119891             18 bp      DNA
DEFINITION   Sequence 19 from patent US 6153424.
ACCESSION    AR119891
VERSION      AR119891.1  GI:14102590
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Raymond,C.K.
TITLE        Protease-deficient strains of Pichia methanolica
JOURNAL      Patent: US 6153424-A 19 28-NOV-2000;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0
US-09-966-880A-8 (1-198) x AR119891 (1-18)
QY           125 GlyLeuArgArgLeu 129
Db           2 GGTCTACGAGGCTC 16
RESULT 117
LOCUS       AR128108             18 bp      DNA
DEFINITION   Sequence 17 from patent US 6183953.
ACCESSION    AR128108
VERSION      AR128108.1  GI:14115770
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Raymond,C.K.
TITLE        Protease-deficient strains of Pichia methanolica
JOURNAL      Patent: US 6183953-A 172 09-JAN-2001;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0
US-09-966-880A-8 (1-198) x AR124397 (1-18)
QY           32 ValValIysArgArg 36
Db           2 GTTGTAAACGACGG 16
RESULT 116
LOCUS       AR124397             18 bp      DNA
DEFINITION   Sequence 172 from patent US 6171859.
ACCESSION    AR124397
VERSION      AR124397.1  GI:14109758
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Herrnstadt,C. and Parker,W.Davis.
TITLE        Method of targeting conjugate molecules to mitochondria
JOURNAL      Patent: US 6171859-A 172 09-JAN-2001;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0
US-09-966-880A-8 (1-198) x AR124397 (1-18)
QY           125 GlyLeuArgArgLeu 129
Db           2 GGTCTACGAGGCTC 16
RESULT 117
LOCUS       AR128108             18 bp      DNA
DEFINITION   Sequence 17 from patent US 6183953.
ACCESSION    AR128108
VERSION      AR128108.1  GI:14115770
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Raymond,C.K.
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TITLE Chromosomal mutagenesis in *Pichia methanolica*
JOURNAL Patent: US 6183953-A 17 06-FEB-2001;
FEATURES Location/Qualifiers

source

1. .18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR128108 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 118

AR138197

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR138197 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR174617 (1-18)

Qy 32 ValVallysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 119

AR174617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .18

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 18

Pred. No.: 8.33e+03 Length: 18

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query

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apoptosis-2.
ACCESSION   BD234560
VERSION     BD234560.1 GI:33044330
KEYWORDS    JP 2002531102-A/42.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Bennett,F.C., Ackermann,E.J. and Cowser,L.M.
TITLE       Antisense modulation of expression of cellular inhibitor of
JOURNAL     Patent: JP 2002531102-A 42 24-SEP-2002;
COMMENT     ISIS PHARMACEUTICALS INC
OS          JP 2002531102-A/42
PD          24-SEP-2002
PF          23-SEP-1999 JP 2000585449
PI          03-DEC-1998 US 09/205144
PI          FRANK C BENNETT,ELIZABETH J ACKERMANN,LEX M COWSERT PC
C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K31/713,A61K48/ PC
00,
PC          A61P35/00,A61P37/00,C12N15/00
CC          Synthetic
FH          Key
FT          source
FEATURES    Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:       0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x BD234560 (1-18)

Qy          38 SerAlaThrSerPhe 42
Db          4 AGTGCTACCTCTTTT 18

RESULT 122
BD237570
LOCUS       Cytokine receptor ZALPHA11.
DEFINITION BD237570
ACCESSION   BD237570.1 GI:33047340
VERSION     JP 2002526062-A/4.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Presnell,S.R., Conklin,D.C., Novak,J.B. and Hammond,A.K.
TITLE       Cytokine receptor ZALPHA11
JOURNAL     Patent: JP 2002526062-A 4 20-AUG-2002;
COMMENT     ZYMOGENETICS INC
OS          JP 2002526062-A/4
PD          20-AUG-2002
PF          23-SEP-1999 JP 2000574143
PI          06-JUL-1999 US 09/159254,09-MAR-1999 US 09/265117 PR
PI          SCOTT R PRESNELL,DARRELL C CONKLIN,JULIA E NOVAK,ANGELA K PI
HAMMOND
PC          C12N15/09,C07K14/715,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC          C12P21/02,C12P21/08,C12Q1/02,G01N33/53,G01N33/566,C12N15/00,
PC          C12N5/00

us-09-966-880a-8 (1-198) x BD237570 (1-18)
Qy          32 ValVallylsArgArg 36
Db          2 GTTGTAAACGACGG 16

RESULT 123
BD237997
LOCUS       Gastric polypeptide ZSIG28.
DEFINITION BD237997
ACCESSION   BD237997.1 GI:33047767
VERSION     JP 2002524103-A/6.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Sheppard,P.O. and Foley,K.P.
TITLE       Gastric polypeptide ZSIG28
JOURNAL     Patent: JP 2002524103-A 6 06-AUG-2002;
COMMENT     ZYMOGENETICS INC
OS          JP 2002524103-A/6
PD          06-AUG-2002
PF          14-SEP-1999 JP 2000570197
PI          16-SEP-1998 US 09/154444
PI          PAUL O SHEPPARD,KEVIN P FOLEY
PC          C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P1/04,A61P1/14, PC
A61P3/08,
PC          A61P5/50,A61P31/04,A61P31/10,A61P35/00,C07K14/47,C07K16/18, PC
C12N1/15,
PC          C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02 PC
,C12Q1/68,G01N33/15,
PC          G01N33/50,G01N33/53,G01N33/577,C12N15/00,C12N5/00,A61K37/02 CC
Oligonucleotide primer ZC976
FH          Key
FT          source
FEATURES    Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:       0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x BD237997 (1-18)
Qy          32 ValVallylsArgArg 36
Db          2 GTTGTAAACGACGG 16

RESULT 124
BD237997
LOCUS       Gastric polypeptide ZSIG28.
DEFINITION BD237997
ACCESSION   BD237997.1 GI:33047767
VERSION     JP 2002524103-A/6.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Sheppard,P.O. and Foley,K.P.
TITLE       Gastric polypeptide ZSIG28
JOURNAL     Patent: JP 2002524103-A 6 06-AUG-2002;
COMMENT     ZYMOGENETICS INC
OS          JP 2002524103-A/6
PD          06-AUG-2002
PF          14-SEP-1999 JP 2000570197
PI          16-SEP-1998 US 09/154444
PI          PAUL O SHEPPARD,KEVIN P FOLEY
PC          C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61P1/04,A61P1/14, PC
A61P3/08,
PC          A61P5/50,A61P31/04,A61P31/10,A61P35/00,C07K14/47,C07K16/18, PC
C12N1/15,
PC          C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02 PC
,C12Q1/68,G01N33/15,
PC          G01N33/50,G01N33/53,G01N33/577,C12N15/00,C12N5/00,A61K37/02 CC
Oligonucleotide primer ZC976
FH          Key
FT          source
FEATURES    Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%         Indels:       0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x BD237997 (1-18)
Qy          32 ValVallylsArgArg 36
Db          2 GTTGTAAACGACGG 16

```

```

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 124
BD244729/C
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Isolation method of primer extension products by modular
oligonucleotide.
ACCESSION BD244729
VERSION BD244729.1 GI:33054499
KEYWORDS JP 2002525076-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lundberg, J. and Uhlen, M.
TITLE Isolation method of primer extension products by modular
JOURNAL Patent: JP 2002525076-A 8 13-AUG-2002;
COMMENT DYNAL AS
OS Artificial Sequence
PN JP 2002525076-A/8
PD 13-AUG-2002
PF 15-SEP-1998 US 09/153242.16-SEP-1998 GB 9820185.8 PI
PR 15-SEP-1998 US 09/153242.16-SEP-1998 GB 9820185.8 PI
JOAKIM LUNDBERG, MATHIAS UHLEN
PC C12N15/09, C12Q1/68, C12N15/00
CC Description of Artificial Sequence: Synthetic oligonucleotide
-
CC pUC18/pRIT28, forward, modulating module, generic FH Key
LOCUS Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD244729 (1-18)

QY 32 ValVallysArgArg 36
Db 17 GTTGTAAACGACGG 3

RESULT 125
BD248283
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Polypeptide zsig58 of pancreas and ovary.
ACCESSION BD248283
VERSION BD248283.1 GI:33058053
KEYWORDS JP 2002524043-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shepard, P.O. and Chandrasekhar, Y.
TITLE Polypeptide zsig58 of pancreas and ovary
JOURNAL Patent: JP 2002524043-A 3 06-AUG-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002524043-A/3
PD 06-AUG-2002

PF 03-AUG-1999 JP 2000563779
PR 03-AUG-1998 US 09/128372
PI PAUL O SHEPPARD, YASMIN CHANDRASEKHAR
PC C12N15/09, C07K14/47, C07K16/46, C07K19/00, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/02, G01N33/15, PC
G01N33/50//
PC (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), C12N15/00, C12N5/00
CC Oligonucleotide primer: ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD248283 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 126
BD249010
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION BD249010
VERSION BD249010.1 GI:33058780
KEYWORDS JP 2002537839-A/71.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak, J.E., Presnell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D.,
Gross, J.A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and
Hammond, A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 71 12-NOV-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002537839-A/71
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908, 11-MAR-1999 US 09/265992 PR
PI JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,
PI RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON,
PI STACEY R DILLON, ANGELA K HAMMOND
PC C12N15/09, A61K38/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52,
PC C07K14/53,
PC C07K14/54, C07K14/55, C07K16/24, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..18
/organism='synthetic construct'

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Db 4 CTTTATTCTTAGA 18
/mmol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD249010 (1-18)

QY 32 ValVallyeArgArg 36
|||||
Db 2 GTTGTAACGACGG 16
|||||

RESULT 127
BD250606
LOCUS
DEFINITION
BD250606 18 bp DNA linear PAT 17-JUL-2003
Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation.
ACCESSION
BD250606.1 GI:33060376
VERSION
JP 2002511276-A/160.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
ORGANISM
1 (bases 1 to 18)
REFERENCE
Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
AUTHORS
Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation.
TITLE
Patent: JP 2002511276-A 160 16-APR-2002;
JOURNAL
ISIS PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2002511276-A/160
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASMOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/30,G06F17/50,PC
C12N15/00
CC Antisense Oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD250606 (1-18)

QY 59 LeuLeupheArg 63
|||||

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Db 4 CTTTATTCTTAGA 18
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD249010 (1-18)

QY 32 ValVallyeArg 36
|||||
Db 2 GTTGTAACGACGG 16
|||||

RESULT 127
BD250606
LOCUS
DEFINITION
BD250606 18 bp DNA linear PAT 17-JUL-2003
Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation.
ACCESSION
BD250606.1 GI:33060376
VERSION
JP 2002511276-A/160.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
ORGANISM
1 (bases 1 to 18)
REFERENCE
Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
AUTHORS
Identification of genetic targets for modulation by
oligonucleotides and generation of oligonucleotides for gene
modulation.
TITLE
Patent: JP 2002511276-A 160 16-APR-2002;
JOURNAL
ISIS PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2002511276-A/160
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASMOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/30,G06F17/50,PC
C12N15/00
CC Antisense Oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD250606 (1-18)

QY 59 LeuLeupheLeuArg 63
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TITLE Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
Identification of genetic targets for modulation by oligonucleotides and generation of oligonucleotides for gene modulation

JOURNAL Patent: JP 2002511276-A 241 16-APR-2002;
ISIS PHARMACEUTICALS INC

COMMENT OS Artificial Sequence
PN JP 2002511276-A/241
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M CONSERV,RENDIA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASMOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/70,G06F17/30,G06F17/50, PC
C12N15/00
CC Identification of genetic targets for modulation by CC
oligonucleotides and
CC generation of oligonucleotides for gene modulation FH Key
Location/Qualifiers
FT source 1. .18
FT Location/Qualifiers
/organism='Artificial Sequence'.
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD250687 (1-18)

QY 103 AsnLeuSerLeuArg 107
Db 17 AACCTTCTCTCAGA 3

RESULT 130
BD251856
LOCUS RING finger protein ZAP03. 18 bp DNA linear PAT 17-JUL-2003
DEFINITION
ACCESSION BD251856
VERSION BD251856.1 GI:33061626
KEYWORDS JP 2002530061-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Venezia,D. and Grossmann,A.
TITLE RING finger protein ZAP03
JOURNAL Patent: JP 2002530061-A 10 17-SEP-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002530061-A/10
PD 17-SEP-2002
PF 04-NOV-1999 JP 2000582416
PR 12-NOV-1998 US 09/191500
PI DOMENICK VENEZIA, ANGELIKA GROSSMANN
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12Q1/02/C12P21/08,C12N15/00,C12N5/00 CC
Oligonucleotide primer ZC976
FH Key Location/Qualifiers
FT source 1. .18

FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD251856 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 131
BD272777
LOCUS Adipocyte-specific protein homolog ZACRP3. 18 bp DNA linear PAT 17-JUL-2003
DEFINITION
ACCESSION BD272777
VERSION BD272777.1 GI:33082545
KEYWORDS JP 2002541847-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte-specific protein homolog ZACRP3
JOURNAL Patent: JP 2002541847-A 13 10-DEC-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002541847-A/13
PD 10-DEC-2002
PF 19-APR-2000 JP 2000612456
PR 20-APR-1999 US 09/294943
PI CHRISTOPHER S PIDDINGTON, PAUL D BISHOP
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/53,G01N33/577,
PC C12N15/00,
PC C12N5/00
CC Oligonucleotide ZC976
FH Key Location/Qualifiers
FT source 1. .18
FT Location/Qualifiers
/organism="Artificial Sequence".
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD272777 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

LOCUS	194960	18 bp	DNA	linear	PAT 01-DEC-1999
DEFINITION	Sequence 1123 from patent US 5731295.				
ACCESSION	I94960				
VERSION	I94960.1				
KEYWORDS	GI:3939430				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.				
TITLE	Method of reducing streptomycin RNA via ribozymes				
JOURNAL	Patent: US 5731295-A 1123 24-MAR-1998;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.33e+03	Length:	18		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x I94960 (1-18)					
Qy	119 ArgLysAlaGluPro 123				
Db	15 AGAAGGCGGACCG 1				
RESULT 135					
AR194048					
LOCUS	AR194048	18 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 20 from patent US 6348331.				
ACCESSION	AR194048				
VERSION	AR194048.1				
KEYWORDS	GI:20240640				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Raymond,C.K.				
TITLE	Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 2				
JOURNAL	Promoter. Patent: US 6348331-A 20 19-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.33e+03	Length:	18		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR194048 (1-18)					
Qy	32 ValValLysArgArg 36				
Db	2 GTTGTAACACGACCG 16				
RESULT 136					
AR207354					
LOCUS	AR207354	18 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 10 from patent US 6372889.				
ACCESSION	AR207354				

LOCUS	194960	18 bp	DNA	linear	PAT 01-DEC-1999
DEFINITION	Sequence 1123 from patent US 5731295.				
ACCESSION	I94960				
VERSION	I94960.1				
KEYWORDS	GI:3939430				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.				
TITLE	Method of reducing streptomycin RNA via ribozymes				
JOURNAL	Patent: US 5731295-A 1123 24-MAR-1998;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.33e+03	Length:	18		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x I94960 (1-18)					
Qy	119 ArgLysAlaGluPro 123				
Db	15 AGAAGGCGGACCG 1				
RESULT 135					
AR194048					
LOCUS	AR194048	18 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 20 from patent US 6348331.				
ACCESSION	AR194048				
VERSION	AR194048.1				
KEYWORDS	GI:20240640				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Raymond,C.K.				
TITLE	Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 2				
JOURNAL	Promoter. Patent: US 6348331-A 20 19-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.33e+03	Length:	18		
Score:	5.00	Matches:	5		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	2.53%	Indels:	0		
DB:	6	Gaps:	0		
US-09-966-880A-8 (1-198) x AR194048 (1-18)					
Qy	32 ValValLysArgArg 36				
Db	2 GTTGTAACACGACCG 16				
RESULT 136					
AR207354					
LOCUS	AR207354	18 bp	DNA	linear	PAT 20-JUN-2002
DEFINITION	Sequence 10 from patent US 6372889.				
ACCESSION	AR207354				

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VERSION AR207354.1 GI:21506241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O., Conklin,D.C., Farrah,T.M., Maurer,M.F. and Grossmann,A.
TITLE Soluble protein ZTMPO-1
JOURNAL Patent: US 6372889-A 10 16-APR-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR207354 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 137
LOCUS AR224080 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 12 from patent US 6440697.
ACCESSION AR224080
VERSION AR224080.1 GI:23332738
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Venezia,D. and Grossmann,A.
TITLE Ring finger protein zap03
JOURNAL Patent: US 6440697-A 12 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR224080 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 138
LOCUS AR224401 18 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 20 from patent US 6440720.
ACCESSION AR224401
VERSION AR224401.1 GI:23333178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using
```

```
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K.
TITLE Pichia methanolica glyceraldehyde-3-phosphate dehydrogenase 2
JOURNAL Patent: US 640720-A 20 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR224401 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 139
LOCUS AR243306 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6475781.
ACCESSION AR243306
VERSION AR243306.1 GI:27290496
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mercola,M.K., Deininger,P.L. and Stiles,C.D.
TITLE Trans-dominant suppressor genes for oligomeric proteins
JOURNAL Patent: US 6475781-A 7 05-NOV-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR243306 (1-18)
Qy 59 LeuLeuPheLeuArg 63
Db 17 CTTCCTCTCTCGCA 3
RESULT 140
LOCUS AR255248 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6482592.
ACCESSION AR255248
VERSION AR255248.1 GI:27304297
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
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modular oligonucleotides
 JOURNAL Patent: US 6482592-A 8 19-NOV-2002;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores: Length: 18
 Pred. No.: 8.33e+03
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 2.53%
 Indels: 0
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AR255248 (1-18)

Qy 32 ValVallysArgArg 36
 |||||
 Db 17 GTTGTAACGACGG 3

RESULT 141

LOCUS 18 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 12 from patent US 6482612.
 ACCESSION AR255758
 VERSION AR255758.1 GI:27304877
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Sheppard,P.O. and Humes,J.M.
 TITLE Adipocyte-specific protein homologs
 JOURNAL Patent: US 6482612-A 12 19-NOV-2002;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores: Length: 18
 Pred. No.: 8.33e+03
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 2.53%
 Indels: 0
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AR255758 (1-18)

Qy 32 ValVallysArgArg 36
 |||||
 Db 2 GTTGTAACGACGG 16

RESULT 142

LOCUS 18 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 19 from patent US 6521233.
 ACCESSION AR281831
 VERSION AR281831.1 GI:29717673
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Piddington,C.S. and Bishop,P.D.
 TITLE Adipocyte complement related protein homolog zacr3
 JOURNAL Patent: US 6521233-A 19 18-FEB-2003;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"

ORIGIN /mol_type="genomic DNA"

Alignment Scores: Length: 18
 Pred. No.: 8.33e+03
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 2.53%
 Indels: 0
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AR281831 (1-18)

Qy 32 ValVallysArgArg 36
 |||||
 Db 2 GTTGTAACGACGG 16

RESULT 143

LOCUS 18 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 6619 from patent US 6537751.
 ACCESSION AR294884
 VERSION AR294884.1 GI:31682168
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 6619 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN /mol_type="genomic DNA"

Alignment Scores: Length: 18
 Pred. No.: 8.33e+03
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 2.53%
 Indels: 0
 DB: 6
 Gaps: 0

US-09-966-880A-8 (1-198) x AR294884 (1-18)

Qy 102 ProAnLeuSerLeu 106
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 Db 4 CCAATCTATCCCTC 18

RESULT 144

LOCUS 18 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 10343 from patent US 6537751.
 ACCESSION AR298608
 VERSION AR298608.1 GI:31685892
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 10343 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="genomic DNA"


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Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR298608 (1-18)

QY 34 LysArgArgAspSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 145
LOCUS AR342878 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6576744.
ACCESSION AR342878
VERSION AR342878.1 GI:33738177
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR342878 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 146
LOCUS AR364357 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 10 from patent US 5262866.
ACCESSION AR364357
VERSION AR364357.1 GI:34426820
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Hong,S.-H.
TITLE Method for displaying a plurality of sequential video images in a
JOURNAL multi-screen picture
FEATURES
Patent: US 5262866-A 10 16-NOV-1993;
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR364357 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 147
LOCUS AR374109 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 77 from patent US 6605272.
ACCESSION AR374109
VERSION AR374109.1 GI:40076681
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 77 12-AUG-2003;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR374109 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 148
LOCUS AR392008 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6613547.
ACCESSION AR392008
VERSION AR392008.1 GI:40115784
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Raymond,C.K., Yanaja,E., Miller,B.G. and Sloan,J.S.
TITLE Pichia methanolica glyceraldhyde-3-phosphate dehydrogenase 1
JOURNAL promoter and terminator
FEATURES Patent: US 6613547-A 18 02-SEP-2003;
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

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DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR3922008 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 149
AR399695
LOCUS AR399695 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 19 from patent US 6620909.
ACCESSION AR399695
VERSION AR399695.1 GI:40142170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp2
JOURNAL Patent: US 6620909-A 19 16-SEP-2003;
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="unknown"
    /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR399695 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 150
AR399963
LOCUS AR399963 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 19 from Patent WO0063377.
ACCESSION AR399963
VERSION AR399963.1 GI:11229983
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp3
JOURNAL Patent: WO 0063377-A 19 26-OCT-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Oligonucleotide ZC976"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX039963 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 151
AR399983
LOCUS AR399983 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 19 from Patent WO0063376.
ACCESSION AR399983
VERSION AR399983.1 GI:11229998
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S. and Bishop,P.D.
TITLE Adipocyte complement related protein homolog zacrp2
JOURNAL Patent: WO 0063376-A 19 26-OCT-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Oligonucleotide ZC976"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX039983 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 152
AR395856
LOCUS AR395856 18 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 28 from Patent WO0073459.
ACCESSION AR395856
VERSION AR395856.1 GI:12228964
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Piddington,C.S., West,J.R., Holly,R.D. and Burkhead,S.K.
TITLE Four-helical bundle protein zsig81
JOURNAL Patent: WO 0073459-A 28 07-DEC-2000;
ZymoGenetics, Inc. (US)
FEATURES
    Location/Qualifiers
    source
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Oligonucleotide primer ZC976"

ORIGIN
Alignment Scores:
Pred. No.: 8.33e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

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US-09-966-880A-8 (1-198) x AX055856 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 153

LOCUS AX061885 18 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 18 from Patent WO0078978.
ACCESSION AX061885
VERSION AX061885.1 GI:12539931

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 Miller,B.G., Sloan,J.S., Raymond,C.K. and Vanaaja,E.
Pichia methanolica glyceralddehyde-3-phosphate dehydrogenase 1
promoter and terminator
JOURNAL Patent: WO 0078978-A 18 28-DEC-2000;
ZymoGenetics, Inc. (US) ; Miller, Brady G. (US) ; Sloan, James S. (US)

FEATURES

source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC976"

ORIGIN

Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX061885 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 154

LOCUS AX093416 18 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 20 from Patent WO0118182.
ACCESSION AX093416
VERSION AX093416.1 GI:13509866

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 Raymond,C.K.
Pichia methanolica glyceralddehyde-3-phosphate dehydrogenase 2
promoter and terminator
JOURNAL Patent: WO 0118182-A 20 15-MAR-2001;
ZymoGenetics, Inc. (US)

FEATURES

source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC976"

ORIGIN

Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX093416 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 155

LOCUS AX172752 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 8 from Patent WO0142292.
ACCESSION AX172752
VERSION AX172752.1 GI:14597848

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 Sheppard,P.O.
Secreted polypeptide zsig87
AUTHORS Patent: WO 0142292-A 8 14-JUN-2001;
TITLE ZymoGenetics, Inc. (US)
JOURNAL
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC976"

ORIGIN

Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX172752 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 156

LOCUS AX179621 18 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 44 from Patent WO0146422.
ACCESSION AX179621
VERSION AX179621.1 GI:15132047

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 Presnell,S.R. and Kindsvogel,W.
Cytokine zcyto18
AUTHORS Patent: WO 0146422-A 44 28-JUN-2001;
TITLE ZymoGenetics, Inc. (US)
JOURNAL
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC976"

ORIGIN

Alignment Scores: 8.33e+03 Length: 18
Pred. No.: 5
Score: 5.00 Matches: 5

Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX179621 (1-18)

Qy 32 ValVallysArgArg 36
 Db 2 GTTGTAAACGACGG 16
 |||||
 |||||

RESULT 157

AX233363 AX233363 18 bp DNA linear PAT 11-SEP-2001
 LOCUS
 DEFINITION Sequence 6 from Patent WO0162788.

ACCESSION AX233363
 VERSION AX233363.1 GI:15592697

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
 TITLE Corneodesmosin based test and model for inflammatory disease
 JOURNAL Patent: WO 0162788-A 6 30-AUG-2001;
 Oxagen Limited (GB)

FEATURES
 Location/Qualifiers
 source
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"

ORIGIN

Alignment Scores:
 Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233363 (1-18)

Qy 129 LeuHisArgAlaGly 133
 Db 3 CTCACAGAGCTGGA 17
 |||||
 |||||

RESULT 158

AX233461 AX233461 18 bp DNA linear PAT 11-SEP-2001
 LOCUS
 DEFINITION Sequence 104 from Patent WO0162788.

ACCESSION AX233461
 VERSION AX233461.1 GI:15592892

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
 TITLE Corneodesmosin based test and model for inflammatory disease
 JOURNAL Patent: WO 0162788-A 104 30-AUG-2001;
 Oxagen Limited (GB)

FEATURES
 Location/Qualifiers
 source
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"

ORIGIN

Alignment Scores:

Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233461 (1-18)

Qy 129 LeuHisArgAlaGly 133
 Db 3 CTCACAGAGCTGGA 17
 |||||
 |||||

RESULT 159

AX233463 AX233463 18 bp DNA linear PAT 11-SEP-2001
 LOCUS
 DEFINITION Sequence 106 from Patent WO0162788.

ACCESSION AX233463
 VERSION AX233463.1 GI:15592898

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
 TITLE Corneodesmosin based test and model for inflammatory disease
 JOURNAL Patent: WO 0162788-A 106 30-AUG-2001;
 Oxagen Limited (GB)

FEATURES
 Location/Qualifiers
 source
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"

ORIGIN

Alignment Scores:
 Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX233463 (1-18)

Qy 129 LeuHisArgAlaGly 133
 Db 3 CTCACAGAGCTGGA 17
 |||||
 |||||

RESULT 160

AX233464 AX233464 18 bp DNA linear PAT 11-SEP-2001
 LOCUS
 DEFINITION Sequence 107 from Patent WO0162788.

ACCESSION AX233464
 VERSION AX233464.1 GI:15592901

KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
 TITLE Corneodesmosin based test and model for inflammatory disease
 JOURNAL Patent: WO 0162788-A 107 30-AUG-2001;
 Oxagen Limited (GB)

FEATURES
 Location/Qualifiers
 source
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer"

ORIGIN

Alignment Scores:

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Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      2.53%      Indels:          0
DB:              6          Gaps:            0

US-09-966-880A-8 (1-198) x AX233464 (1-18)

QY      129 LeuHisArgAlaGly 133
      |||||
Db       3 CTCACAGAGCTGGA 17

RESULT 161
AX548073
LOCUS      AX548073
DEFINITION Sequence 22 from Patent WO0234917.
ACCESSION AX548073
VERSION    AX548073.1 GI:25813168
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Conklin,D.C., Gao,Z., Lofton-Day,C.E. and Whitmore,T.B.
TITLE      Secreted alpha-helical protein zlm2a24
JOURNAL    Patent: WO 0234917-A 22 02-MAY-2002;
           ZymoGenetics, Inc. (US)
FEATURES   Location/Qualifiers
           source
             1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide Sequence ZC976"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      2.53%      Indels:          0
DB:              6          Gaps:            0

US-09-966-880A-8 (1-198) x AX548073 (1-18)

QY      32 ValVallyArgArg 36
      |||||
Db       2 GTTGTAACGACGG 16

RESULT 162
AX713216/c
LOCUS      AX713216
DEFINITION Sequence 102 from Patent WO03018837.
ACCESSION AX713216
VERSION    AX713216.1 GI:29823805
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Waschuetza,S., Schnakenberg,E. and Lustig,M.
TITLE      Method and diagnostic kit for the molecular diagnosis of
           pharmacologically relevant genes
JOURNAL    Patent: WO 03018837-A 102 06-MAR-2003;
           Adnagen AG (DE)
FEATURES   Location/Qualifiers
           source
             1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonukleotid"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      2.53%      Indels:          0
DB:              6          Gaps:            0

US-09-966-880A-8 (1-198) x AX802576 (1-18)

QY      174 ArgGlnLeuArgArg 178
      |||||
Db       18 AGACAGCTCAGAGA 4

RESULT 164
AX802807/c
LOCUS      AX802807
DEFINITION Sequence 317 from Patent WO03057914.
ACCESSION AX802807
VERSION    AX802807.1 GI:38501505
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Karlsen,F.
TITLE      Method for detecting human papillomavirus mRNA
JOURNAL    Patent: WO 03057914-A 317 17-JUL-2003;
           Norchip A/S (NO)
FEATURES   Location/Qualifiers
           source
             1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="HPV primer"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      2.53%      Indels:          0
DB:              6          Gaps:            0

US-09-966-880A-8 (1-198) x AX713216 (1-18)

QY      22 LysGlyArgGlu 26
      |||||
Db       16 AAGGGCAGGAGAG 2

RESULT 163
AX802576/c
LOCUS      AX802576
DEFINITION Sequence 86 from Patent WO03057914.
ACCESSION AX802576
VERSION    AX802576.1 GI:38501274
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Karlsen,F.
TITLE      Method for detecting human papillomavirus mRNA
JOURNAL    Patent: WO 03057914-A 86 17-JUL-2003;
           Norchip A/S (NO)
FEATURES   Location/Qualifiers
           source
             1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="HPV primer"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      2.53%      Indels:          0
DB:              6          Gaps:            0

US-09-966-880A-8 (1-198) x AX802576 (1-18)

QY      174 ArgGlnLeuArgArg 178
      |||||
Db       18 AGACAGCTCAGAGA 4

RESULT 164
AX802807/c
LOCUS      AX802807
DEFINITION Sequence 317 from Patent WO03057914.
ACCESSION AX802807
VERSION    AX802807.1 GI:38501505
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Karlsen,F.
TITLE      Method for detecting human papillomavirus mRNA
JOURNAL    Patent: WO 03057914-A 317 17-JUL-2003;
           Norchip A/S (NO)
FEATURES   Location/Qualifiers
           source
             1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="HPV primer"

ORIGIN

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/note="primer"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX802807 (1-18)

QY 174 ArgGlnLeuArgArg 178
 |||||
 DB 18 AGACAGCTCAGAAGA 4

RESULT 165

AX803113/c AX803113 18 bp DNA linear PAT 24-NOV-2003
 LOCUS Sequence 145 from Patent WO03057927.
 DEFINITION AX803113
 ACCESSION AX803113
 VERSION AX803113.1 GI:38501778
 KEYWORDS Human papillomavirus
 SOURCE Human papillomavirus
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 Papillomavirus.

REFERENCE 1
 AUTHORS Karlsen,F.
 TITLE Detection of human papillomavirus e6 mrna
 JOURNAL Patent: WO 03057927-A 145 17-JUL-2003;
 Norchip A/S (NO)

FEATURES
 source Location/Qualifiers
 1..18
 /organism="Human papillomavirus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10566"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX803113 (1-18)

QY 174 ArgGlnLeuArgArg 178
 |||||
 DB 18 AGACAGCTCAGAAGA 4

RESULT 166

AX803298/c AX803298 18 bp DNA linear PAT 24-NOV-2003
 LOCUS Sequence 330 from Patent WO03057927.
 DEFINITION AX803298
 ACCESSION AX803298
 VERSION AX803298.1 GI:38501963
 KEYWORDS Human papillomavirus
 SOURCE Human papillomavirus
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 Papillomavirus.

REFERENCE 1
 AUTHORS Karlsen,F.
 TITLE Detection of human papillomavirus e6 mrna
 JOURNAL Patent: WO 03057927-A 330 17-JUL-2003;
 Norchip A/S (NO)

FEATURES
 source Location/Qualifiers
 1..18
 /organism="Human papillomavirus"

/mol_type="unassigned DNA"
/db_xref="taxon:10566"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX803298 (1-18)

QY 174 ArgGlnLeuArgArg 178
 |||||
 DB 18 AGACAGCTCAGAAGA 4

RESULT 167

BD006571 BD006571 18 bp DNA linear PAT 31-JAN-2002
 LOCUS Secreted salivary ZSIG32 polypeptides.
 DEFINITION BD006571
 ACCESSION BD006571
 VERSION BD006571.1 GI:18634942
 KEYWORDS JP 2001501834-A/10.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Sheppard,P.O.
 TITLE Secreted salivary ZSIG32 polypeptides
 JOURNAL Patent: JP 2001501834-A 10 13-FEB-2001;
 ZYMOGENETICS INC
 COMMENT OS Unidentified
 PN JP 2001501834-A/10
 PD 13-FEB-2001
 PF 18-MAR-1998 JP 1998540741
 PR 19-MAR-1997 US 60/041263
 PI PAUL O SHEPPARD
 PC C12N15/12,C07K14/47,A61K38/17,C07K16/18,C12Q1/68,C12N15/62, PC
 C12N15/11

PC G01N33/50
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism="Unidentified".
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Alignment Scores: Pred. No.: 8.33e+03 Length: 18
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD006571 (1-18)

QY 32 ValVallysArgArg 36
 |||||
 DB 2 GTTGTAACGACGG 16

RESULT 168

BD073403 BD073403 18 bp DNA linear PAT 27-AUG-2002
 LOCUS Secreted protein which human chromosome 13 encodes.
 DEFINITION BD073403
 ACCESSION BD073403

```

VERSION BD073403.1 GI:22619006
KEYWORDS JP 2001511345-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O. and Gilberton,D.G.
TITLE Secreted protein which human chromosome 13 encodes
JOURNAL Patent: JP 2001511345-A 2 14-AUG-2001;
        ZYMOGENETICS INC
COMMENT OS Artificial Sequence
        PN JP 2001511345-A/2
        PD 14-AUG-2001
        PF 24-JUL-1998 JP 2000504249
        PR 24-JUL-1997 US 60/053613
        PI PAUL O SHEPPARD,DIBRA G GILBERTON
        PC C12N15/09,A61K38/00,A61K48/00,C07K14/47,C07K16/18,C12N1/15,PC
        C12N1/19,
        PC
C12N1/21,C12N5/10,C12P21/02,C13Q1/68,C12N15/00,A61K37/02,C12N5/ PC
00
CC Oligonucleotide ZC976
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
  source      Location/Qualifiers
  1..18       /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:         0
DB:              6           Gaps:           0

US-09-966-880A-8 (1-198) x BD074786 (1-18)

QY      32 ValVallylsargArg 36
Db      2 GTTGTAACGACGG 16

RESULT 170
BD095308
LOCUS      BD095308
DEFINITION The method of testing for psoriasis vulgaris.
ACCESSION  BD095308
VERSION     BD095308.1 GI:22640896
KEYWORDS   WO 0142458-A/13.
SOURCE     synthetic construct
          artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Inoko,H. and Tamiya,G.
TITLE     The method of testing for psoriasis vulgaris
JOURNAL   Patent: WO 0142458-A 13 14-JUN-2001;
          HIDEOSHI INOKO,GEN TAMIYA
COMMENT   OS Artificial Sequence
          PN WO 0142458-A/13
          PD 14-JUN-2001
          PF 06-DEC-2000 WO 2000JP008624
          PR 06-DEC-1999 JP 99P 346867
          PI HIDEOSHI INOKO,GEN TAMIYA
          PC C12N15/12,C12Q1/68
          CC Description of Artificial Sequence:an artificially synthesized

FEATURES
  source      Location/Qualifiers
  1..18       /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:         0
DB:              6           Gaps:           0

US-09-966-880A-8 (1-198) x BD095308 (1-18)

QY      128 ArgLeuHisArgAla 132
Db      4 CGCCTCCACGAGCT 18

RESULT 169
BD074786
LOCUS      BD074786
DEFINITION Homolog of protein specific to adipocyte.
ACCESSION  BD074786
VERSION     BD074786.1 GI:22620389
KEYWORDS   JP 2001513998-A/5.
SOURCE     synthetic construct
          artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Sheppard,P.O. and Humes,J.M.
TITLE     Homolog of protein specific to adipocyte
JOURNAL   Patent: JP 2001513998-A 5 11-SEP-2001;
          ZYMOGENETICS INC
COMMENT   OS Artificial Sequence
        PN JP 2001513998-A/5
        PD 11-SEP-2001
        PF 26-AUG-1998 JP 2000507800
        PR 26-AUG-1997 US 60/056983
        PI PAUL O SHEPPARD,JACQUELINE M HUMES
        PC C12N15/09,A61K38/17,A61K39/395,A61K45/00,A61P3/00,A61P29/00,
        A61P43/00,
        PC C07K14/47,C07K16/18,C12P21/02,C13Q1/68,C12P21/08,C12N15/00,
        A61K37/12
        PC
        CC Oligonucleotide ZC976
        FH Key Location/Qualifiers

```



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Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x BD206032 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 174
LOCUS   BD211410
DEFINITION Immunomodulator polypeptide ZSIG57.
ACCESSION BD211410
VERSION  BD211410.1 GI:33021180
KEYWORDS JP 2002518009-A/3.
SOURCE   synthetic construct
         artificial construct
         artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS   Sheppard,P.O.
TITLE     Immunomodulator polypeptide ZSIG57
JOURNAL   Patent: JP 2002518009-A 3 25-JUN-2002;
COMMENT   ZYMOGENETICS INC
OS       Artificial Sequence
PN       JP 2002518009-A/3
PD       25-JUN-2002
PF       20-MAY-1999 JP 2000554849
PR       18-JUN-1998 US 09/099600
PI       PAUL O SHEPPARD
PC       C12N15/09,C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21, PC
         C12N5/10,
PC       C12B21/08//(C12N1/19,C12R1/84),C12N15/00,C12N5/00 CC
FEATURES   Oligonucleotide primer Zc976
            FH Key      Location/Qualifiers
            FT source    1..18
                        /organism="Artificial Sequence"
            source       1..18
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.:      8.33e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x BD211410 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 175
LOCUS   AR002659
DEFINITION Sequence 20 from patent US 5741957.
ACCESSION AR002659
VERSION  AR002659.1 GI:3964213
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Deboer,H.A., Strijker,R., Heyneker,H.L., Platenburg,G., Lee,S.He.,

US-09-966-880A-8 (1-198) x AR002659 (1-19)

QY      32 ValVallysArgArg 36
Db      5 GTTGTAAACGACGG 19

RESULT 176
LOCUS   AR065110
DEFINITION Sequence 2 from patent US 5849486.
ACCESSION AR065110
VERSION  AR065110.1 GI:5995326
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Heller,M.James., O'Connell,J.Patrick., Juncosa,R.David.,
         Sosnowski,R.George, and Jackson,T.Ratcliffe.
TITLE     Methods for hybridization analysis utilizing electrically
         controlled hybridization
JOURNAL   Patent: US 5849486-A 2 15-DEC-1998;
FEATURES   Location/Qualifiers
            source       1..19
                        /organism="unknown"
                        /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      8.73e+03      Length:      19
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6             Gaps:        0

US-09-966-880A-8 (1-198) x AR065110 (1-19)

QY      56 HisValGluLeuLeu 60
Db      2 CACGTAGAACTGCTC 16

RESULT 177
LOCUS   AR118403
DEFINITION Sequence 20 from patent US 6140552.
ACCESSION AR118403
VERSION  AR118403.1 GI:14099309
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Deboer,H.A., Strijker,R., Heyneker,H.L., Platenburg,G., Lee,S.He.,

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Pieper, P. and Krimpenfort, P.J.A.
Production of recombinant polypeptides by bovine species and
transgenic methods

JOURNAL Patent: US 6140552-A 20 31-OCT-2000;
FEATURES Location/Qualifiers

source

1. .19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 19
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR118403 (1-19)

QY 32 ValVallysArgArg 36

Db 5 GTTGTAAACGACGG 19

RESULT 178

AR153868

LOCUS

DEFINITION Sequence 21 from patent US 6238624. 19 bp DNA linear PAT 08-AUG-2001

ACCESSION AR153868

VERSION AR153868.1 GI:15121921

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Heller, M.J., Tu, E., Evans, G.A. and Sosnowski, R.G.

TITLE Methods for transport in molecular biological analysis and

diagnostics

JOURNAL Patent: US 6238624-A 21 29-MAY-2001;

FEATURES

source Location/Qualifiers

1. .19

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 19
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR153868 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16

RESULT 179

AR157371

LOCUS

DEFINITION Sequence 2 from patent US 6245508. 19 bp DNA linear PAT 17-OCT-2001

ACCESSION AR157371

VERSION AR157371.1 GI:16218306

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Heller, M.James. and Sosnowski, R. George.

TITLE Method for fingerprinting utilizing an electronically addressable

array

JOURNAL Patent: US 6245508-A 2 12-JUN-2001;

FEATURES

source Location/Qualifiers

1. .19

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: 19
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR157371 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16

RESULT 180

E36205/C

LOCUS

DEFINITION

Process for preparing ammonia oxidizing bacterium variant with

limited proliferation in natural environment. 19 bp DNA linear PAT 18-JUN-2001

ACCESSION E36205

VERSION E36205.1 GI:13022532

KEYWORDS JP 1999235188-A/7.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 19)

AUTHORS Taro, I.

TITLE Process for preparing ammonia oxidizing bacterium variant with

limited proliferation in natural environment

JOURNAL Patent: JP 1999235188-A 7 31-AUG-1999;

COMMENT KURIITA WATER IND LTD

OS Unidentified

PN JP 1999235188-A/7

PD 31-AUG-1999

PF 08-DEC-1998 JP 1998349146

PR TARO IZUMI

PC C12N15/09 C12N1/21//C12N9/88, (C12N1/21, C12R1:01), C12N15/00 CC

Strandedness: Single;

CC Topology: Linear;

FT Key

FT source

FT Location/Qualifiers

1. .19

/organism="Unidentified".

FEATURES

source Location/Qualifiers

1. .19

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

ORIGIN

Alignment Scores: 19
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x E36205 (1-19)

QY 32 ValVallysArgArg 36

Db 15 GTTGTAAACGACGG 1

RESULT 181

E37237/C

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x I38407 (1-19)

Qy 56 HieValgluieuLeu 60
Db 18 CACGTAGAACTGTC 4

RESULT 185

LOCUS I43686 19 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 20 from patent US 5633076.
ACCESSION I43686
VERSION I43686.1 GI:2468784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS DeBoer,H.A., Strijker,R., Heyneker,H.L., Platenburg,G., Lee,S.H., Pieper,P. and Krimpenfort,P.J.A.
TITLE Method of producing a transgenic bovine or transgenic bovine embryo
JOURNAL Patent: US 5633076-A 20 27-MAY-1997;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: Length: 19
Pred. No.: 8.73e+03 Matches: 5
Score: 5.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x I43686 (1-19)

Qy 32 ValVallysArgArg 36
Db 5 GTTGTHAAGCAGCG 19

RESULT 186

LOCUS I79524 19 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 15 from patent US 5707809.
ACCESSION I79524
VERSION I79524.1 GI:3207814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Halverson,J. and Dvorak,J.
TITLE Avian sex identification probes
JOURNAL Patent: US 5707809-A 15 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: Length: 19
Pred. No.: 8.73e+03 Matches: 5
Score: 5.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x I79524 (1-19)

Qy 82 ThrSerTipSerPro 86
Db 17 ACAGCTGGAGCCCA 3

RESULT 187

LOCUS I88976 19 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 18 from patent US 5719271.
ACCESSION I88976
VERSION I88976.1 GI:3408916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Bruce,T.
TITLE Covalently cross-linked oligonucleotides
JOURNAL Patent: US 5719271-A 18 17-FEB-1998;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores: Length: 19
Pred. No.: 8.73e+03 Matches: 5
Score: 5.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x I88976 (1-19)

Qy 179 IleLeuLeuProLeu 183
Db 17 ATTCTCTACTCTCTG 3

RESULT 188

LOCUS AR222934 19 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 44 from patent US 6432639.
ACCESSION AR222934
VERSION AR222934.1 GI:23330771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Lichter,J.B. and Guida,M.
TITLE Isolated CYP3A4 nucleic acid molecules and detection methods
JOURNAL Patent: US 6432639-A 44 13-AUG-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores: Length: 19
Pred. No.: 8.73e+03 Matches: 5
Score: 5.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR222934 (1-19)

Qy 22 LysGlyArgArgGlu 26
Db 3 AAGGCGAGAGAGAG 17

RESULT 189

```
AR364956/c
LOCUS AR364956 19 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5455029.
ACCESSION AR364956
VERSION AR364956.1 GI:34428177
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hartman,J.R., Oppenheim,A.B., Gorecki,M., Aviv,H. and Oren,R.
TITLE Therapeutic compositions comprising a mixture of human CuZn superoxide dismutase analogs
JOURNAL Patent: US 5455029-A 5 03-OCT-1995;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53% Mismatches: 0
DB: 6 Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AR364956 (1-19)
QY 69 AspLeuAspProGly 73
Db 18 GATCTAGACCGGGA 4
RESULT 190
AR364974/c
LOCUS AR364974 19 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 25 from patent US 5455029.
ACCESSION AR364974
VERSION AR364974.1 GI:34428195
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hartman,J.R., Oppenheim,A.B., Gorecki,M., Aviv,H. and Oren,R.
TITLE Therapeutic compositions comprising a mixture of human CuZn superoxide dismutase analogs
JOURNAL Patent: US 5455029-A 25 03-OCT-1995;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53% Mismatches: 0
DB: 6 Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AR364974 (1-19)
QY 69 AspLeuAspProGly 73
Db 18 GATCTAGACCGGGA 4
RESULT 191
AR430797
LOCUS AR430797 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 100 from patent US 6649409.
ACCESSION AR430797
VERSION AR430797.1 GI:40191726
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Fomsgaard,A.
TITLE Method for producing a nucleotide sequence construct with optimized codons for an HIV genetic vaccine based on a primary, early HIV isolate and synthetic envelope BX08 constructs
JOURNAL Patent: US 6649409-A 100 18-NOV-2003;
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53% Mismatches: 0
DB: 6 Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AR430797 (1-19)
QY 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15
RESULT 192
AXI29047
LOCUS AXI29047 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 265 from Patent WO0130362.
ACCESSION AXI29047
VERSION AXI29047.1 GI:14135352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 265 03-MAY-2001;
FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk2 ribozyme binding site"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53% Mismatches: 0
DB: 6 Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AXI29047 (1-19)
QY 193 PheArgThrLeuGly 197
Db 1 TTTCGGACTCTGGGG 15
RESULT 193
AXI30454
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LOCUS AX130454 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1672 from Patent WO0130362.
ACCESSION AX130454
VERSION AX130454.1 GI:14136759
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1672 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin C ribozyme binding site"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX130454 (1-19)
QY 62 LeuArgTyrIleSer 66
Db 3 CTACGGTATATTCA 17
RESULT 194
AX130455
LOCUS AX130455 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1673 from Patent WO0130362.
ACCESSION AX130455
VERSION AX130455.1 GI:14136760
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1673 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin C ribozyme binding site"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX130455 (1-19)
QY 62 LeuArgTyrIleSer 66
Db 3 CTACGGTATATTCA 17

LOCUS AX130454 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1672 from Patent WO0130362.
ACCESSION AX130454
VERSION AX130454.1 GI:14136759
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1672 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin C ribozyme binding site"
ORIGIN
Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX130454 (1-19)
QY 62 LeuArgTyrIleSer 66
Db 3 CTACGGTATATTCA 17

LOCUS AX130455 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1673 from Patent WO0130362.
ACCESSION AX130455
VERSION AX130455.1 GI:14136760
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1673 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin C ribozyme binding site"
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Alignment Scores: 8.73e+03 Length: 19
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX130455 (1-19)
QY 62 LeuArgTyrIleSer 66
Db 3 CTACGGTATATTCA 17

LOCUS AX421255 19 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 3 from Patent WO0218641.
ACCESSION AX421255
VERSION AX421255.1 GI:21524663
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risinger, C., Andersson, M.K., Lewander, T. and Claissan, E.
TITLE Detection of CYP3A4 and CYP2C9 polymorphisms
JOURNAL Patent: WO 0218641-A 3 07-MAR-2002;
Geminl Genomics PLC (GB)
FEATURES source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide of CYP3A4 region"
ORIGIN
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Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX421255 (1-19)
QY 22 LysGlyArgArgGlu 26
Db 3 AAGGGCAGGAGAGAG 17
RESULT 196
AX497578
LOCUS AX497578 19 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 122 from Patent WO0233126.
ACCESSION AX497578
VERSION AX497578.1 GI:23342848
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Grenier, J.K., Marshall, D.J., Prudent, J.R., Richmond, C.S.,
Roesch, E.B., Scherrer, C.W., Sherrill, C.B. and Ptacin, J.L.
TITLE Solid support assay systems and methods utilizing non-standard bases
JOURNAL Patent: WO 0233126-A 122 25-APR-2002;
Eragen Biosciences, Inc. (US)
FEATURES source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotides"
ORIGIN
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Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6
US-09-966-880A-8 (1-198) x AX421255 (1-19)
QY 22 LysGlyArgArgGlu 26
Db 3 AAGGGCAGGAGAGAG 17

US-09-966-880A-8 (1-198) x AX497578 (1-19)

QY 111 AlaArgLeuTyrPhe 115
 Db 1 GCAAGGCTCTACTTC 15

RESULT 197

AX708353
 LOCUS AX708353 19 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 12 from Patent WO02074952.
 ACCESSION AX708353
 VERSION AX708353.1 GI:29564240
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Merk, H. and Stiege, W.
 TITLE Nucleic acid which is stabilised against decomposition
 JOURNAL Patent: WO 02074952-A 12 26-SEP-2002;
 Rina Network RNA-Technologien GmbH (DE)
 FEATURES Location/Qualifiers
 source
 primer_bind
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.73e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX708353 (1-19)

QY 32 ValVallysArgArg 36
 Db 5 GTTGTAACGACGG 19

RESULT 198

AX708367
 LOCUS AX708367 19 bp DNA linear PAT 04-APR-2003
 DEFINITION Sequence 12 from Patent WO02090371.
 ACCESSION AX708367
 VERSION AX708367.1 GI:29564254
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Merk, H., Erdmann, V. and Stiege, W.
 TITLE Method for preparative production of long nucleic acids by PCR
 JOURNAL Patent: WO 02090371-A 12 14-NOV-2002;
 Rina Network RNA-Technologien GmbH (DE)
 FEATURES Location/Qualifiers
 source
 primer_bind
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.73e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX708367 (1-19)

QY 32 ValVallysArgArg 36
 Db 5 GTTGTAACGACGG 19

RESULT 199

AX710980
 LOCUS AX710980 19 bp RNA linear PAT 11-APR-2003
 DEFINITION Sequence 280 from Patent EP1288296.
 ACCESSION AX710980
 VERSION AX710980.1 GI:29787361
 KEYWORDS Human herpesvirus 5
 SOURCE Human herpesvirus 5
 ORGANISM Human herpesvirus 5
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Betaherpesvirinae; Cytomegalovirus.
 REFERENCE 1
 AUTHORS Draper, K.G., Mcswiggen, J.A., Holecsek, J.J., Dudycz, L.W.,
 Macejak, D.G. and Mamone, J.A.
 TITLE Method and reagent for inhibiting HBV viral replication
 JOURNAL Patent: EP 1288296-A 280 05-MAR-2003;
 RIBOZYME PHARMACEUTICALS, INC. (US)
 FEATURES Location/Qualifiers
 source
 primer_bind
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.73e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AX710980 (1-19)

QY 124 GluGlyLeuArgArg 128
 Db 1 GAAGGCTACGCGT 15

RESULT 200

BD001121
 LOCUS BD001121 19 bp RNA linear PAT 31-JAN-2002
 DEFINITION Method and reagent for inhibiting viral replication.
 ACCESSION BD001121
 VERSION BD001121.1 GI:18625680
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Draper, K.G., Dadykzt, L.W., Macswiggen, J.A., Maysejak, D.G.,
 Holecsek, J.J. and Mamone, A.J.
 TITLE Method and reagent for inhibiting viral replication
 JOURNAL Patent: JP 2000342285-A 281 12-DEC-2000;
 RIBOZYME PHARMACEUTICALS INC
 COMMENT OS Artificial Sequence
 PN JP 2000342285-A/281
 PD 12-DEC-2000
 PR 01-MAY-2000 JP 2000132616
 PF 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
 14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
 14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
 14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
 14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
 14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
 14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
 14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR

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14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00,C12N9/22/(C12N5/10,C12R1:91), PC
C12N15/00,
CC C12N5/00,(C12N5/00,C12R1:91)
FH Key Location/Qualifiers
FT source 1..19 /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
ORIGIN
1..19
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x BD001121 (1-19)
QY 124 GluclyleuArgArg 128
DB 1 GAAGGCTACCGCT 15
RESULT 201
BD001550
LOCUS 19 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001550
VERSION BD001550.1 GI:18626109
KEYWORDS JP 2000342286-A/281.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 281 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342286-A/281
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/882923 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/935854 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/948359 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,

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PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00/(A61K38/43,A61K39/125,A61K39/13,
A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
A61P1/16,
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12O1/68, PC
(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC
FH Key Location/Qualifiers
FT source 1..19 /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
ORIGIN
1..19
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Alignment Scores:
Pred. No.: 8.73e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x BD001550 (1-19)
QY 124 GluclyleuArgArg 128
DB 1 GAAGGCTACCGCT 15
RESULT 202
BD087510
LOCUS 19 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION BD087510
VERSION BD087510.1 GI:22633120
KEYWORDS JP 2001525193-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 19)
AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
Edman,C.F.
TITLE Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL Patent: JP 2001525193-A 21 11-DEC-2001;
NANOGEN INC
COMMENT OS Homo sapiens (human)
PN JP 2001525193-A/21
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1987 US 08/986065
PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER,CARL F EDMAN
PC C12O1/68,C12N15/09,C12N15/00
CC Self-assembling microelectronic integration system capable of
designating
CC self address, compartment device, mechanism, method and CC
operation for
CC molecular biological analysis and diagnosis
FH Key Location/Qualifiers
FT source 1..19 /organism='Homo sapiens (human)'.
FEATURES
source Location/Qualifiers
1..19

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:      8.73e+03      Length:      19
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6            Gaps:          0

US-09-966-880A-8 (1-198) x BD087510 (1-19)

Qy      56 HisValGluLeuLeu 60
Db      2 CACGTAGACTGCTC 16

RESULT 203
BD087534/c
LOCUS
DEFINITION
Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION
BD087534
VERSION
BD087534.1 GI:22633144
KEYWORDS
JP 2001525193-A/45.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 19)
AUTHORS
Edman, C.F.
TITLE
Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL
NANOGEN INC
COMMENT
OS Homo sapiens (human)
PN JP 2001525193-A/45
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER, CARL F EDMAN
PC C1201/68, C12N15/09, C12N15/00
CC Self-assembling microelectronic integration system capable of
designating
CC self address, compartment device, mechanism, method and CC
operation for
CC molecular biological analysis and diagnosis
FH Key Location/Qualifiers
FT source 1..19
/organism="Homo sapiens (human)"
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Alignment Scores:
Pred. No.:      8.73e+03      Length:      19
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6            Gaps:          0

US-09-966-880A-8 (1-198) x BD087534 (1-19)

Qy      56 HisValGluLeuLeu 60
Db      2 CACGTAGACTGCTC 16

RESULT 204
BD087539/c
LOCUS
DEFINITION
Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis.
ACCESSION
BD087539
VERSION
BD087539.1 GI:22633149
KEYWORDS
JP 2001525193-A/50.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 19)
AUTHORS
Edman, C.F.
TITLE
Self-assembling microelectronic integration system capable of
designating self address, compartment device, mechanism, method and
operation for molecular biological analysis and diagnosis
JOURNAL
NANOGEN INC
COMMENT
OS Homo sapiens (human)
PN JP 2001525193-A/50
PD 11-DEC-2001
PF 01-DEC-1998 JP 2000524303
PR 05-DEC-1997 US 08/986065
PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
NERENBERG,
PI MICHAEL J HELLER, CARL F EDMAN
PC C1201/68, C12N15/09, C12N15/00
CC Self-assembling microelectronic integration system capable of
designating
CC self address, compartment device, mechanism, method and CC
operation for
CC molecular biological analysis and diagnosis
FH Key Location/Qualifiers
FT source 1..19
/organism="Homo sapiens (human)"
FEATURES
source
1..19
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/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.:      8.73e+03      Length:      19
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%         Indels:        0
DB:             6            Gaps:          0

US-09-966-880A-8 (1-198) x BD087539 (1-19)

Qy      56 HisValGluLeuLeu 60
Db      18 CACGTAGACTGCTC 4

RESULT 205
A00694
LOCUS
DEFINITION
Artificial sequence for controllable repressor operator (HO -150).
ACCESSION
A00694
VERSION
A00694.1 GI:344205
KEYWORDS
synthetic construct
SOURCE
ORGANISM
synthetic construct

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artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE EUCARYOTIC EXPRESSION VECTORS
JOURNAL Patent: WO 860926-A 13 13-FEB-1986;
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A00694 (1-20)

QY 192 AlapheArgThrLeu 196
Db 1 GCGTTTAGACGCTT 15

RESULT 206
LOCUS A07599/c 20 bp DNA linear
DEFINITION Synthetic antisense oligonucleotide (5604-5623).
ACCESSION A07599
VERSION A07599.1 GI:413102
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Stropp,U., Baumgarten,J., Loebberding,A., Springer,W., Piel,N.,
Kretschmer,A., Koelbl,H. and Frommer,W.
TITLE Antisense-oligonucleotides for inhibiting the transactivator target
sequence (TAR) and the synthesis of the transactivator protein
(Tat) of HIV-1, and their use
JOURNAL Patent: EP 0386563-A 6 12-SEP-1990;
BAYER AG
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A07599 (1-20)

QY 10 LysPheLeuTVrGln 14
Db 17 AAGTTTCTCTATCAA 3

RESULT 207
LOCUS A32719 20 bp DNA linear
DEFINITION Synthetic capture probe for HPV6/HPV11 E7 gene.
ACCESSION A32719
VERSION A32719.1 GI:11567567
KEYWORDS
SOURCE
synthetic construct

artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS
TITLE EUCARYOTIC EXPRESSION VECTORS
JOURNAL Patent: WO 860926-A 13 13-FEB-1986;
FEATURES Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A32719 (1-20)

QY 174 ArgGlnLeuArgArg 178
Db 1 AGACAGCTCAGAAGA 15

RESULT 208
LOCUS A45733 20 bp DNA linear
DEFINITION Sequence 12 from Patent WO9520668.
ACCESSION A45733
VERSION A45733.1 GI:2300120
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul,W., Scott,R.J., Betzner,A., Huttner,E., Lenee,P. and Perez,P.
TITLE METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
JOURNAL Patent: WO 9520668-A 12 03-AUG-1995;
NICKERSON BIOCEM LTD (GB)
COMMENT Other publication CA 2182278 950803
Other publication AU 1540995 950815.
FEATURES
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1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x A45733 (1-20)

QY 32 ValVallyArgArg 36
Db 2 GTTGTAACACGCGG 16

RESULT 209
LOCUS A45737 20 bp DNA linear
DEFINITION Sequence 16 from Patent WO9520668.
ACCESSION A45737
VERSION A45737.1 GI:2300124
KEYWORDS

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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul, W., Scott, R.J., Betzner, A., Huttner, E., Lensee, P. and Perez, P.
TITLE METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
JOURNAL PATENT: WO 9520668-A 16 03-AUG-1995;
NICKERSON BIOCEM LTD (GB)
COMMENT Other publication CA 2182278 950803
Other publication AU 1540995 950815.
FEATURES Location/Qualifiers
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1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x A45737 (1-20)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 210
A45739
LOCUS A45739 20 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 18 from Patent WO9520668.
ACCESSION A45739
VERSION A45739.1 GI:2300126
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul, W., Scott, R.J., Betzner, A., Huttner, E., Lensee, P. and Perez, P.
TITLE METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
JOURNAL PATENT: WO 9520668-A 16 03-AUG-1995;
NICKERSON BIOCEM LTD (GB)
COMMENT Other publication CA 2182278 950803
Other publication AU 1540995 950815.
FEATURES Location/Qualifiers
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x A45739 (1-20)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 211
A47817
LOCUS A47817 20 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 31 from Patent WO9533851.

ACCESSION A47817
VERSION A47817.1 GI:2301703
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS De.B.H., Portaeis, F., Machtelincx, J., Jannes, G. and Rossau, R.
TITLE METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
JOURNAL PATENT: WO 9533851-A 31 14-DEC-1995;
INNOGENETICS NV (BE)
COMMENT Other publication AU 2789695 960104.
FEATURES Location/Qualifiers
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x A47817 (1-20)
QY 92 ArgHisValAlaAsp 96
Db 4 CGGCATGTCGGCAT 18
RESULT 212
AR011896/c
LOCUS AR011896 20 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 49 from patent US 5763174.
ACCESSION AR011896
VERSION AR011896.1 GI:3969886
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nishikura, K.
TITLE RNA editing enzyme and methods of use thereof
JOURNAL PATENT: US 5763174-A 49 09-JUN-1998;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0
US-09-966-880A-8 (1-198) x AR011896 (1-20)
QY 38 SerAlaThrSerPhe 42
Db 17 TCAGCCACATCCTTC 3
RESULT 213
AR020656/c
LOCUS AR020656 20 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 44 from patent US 5789184.
ACCESSION AR020656

VERSION AR020656.1 GI:3975271
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fowlkes,D.M., Broach,J., Manfredi,J., Klein,C., Murphy,A.J., Paul,J. and Truheart,J.
TITLE yeast cells engineered to produce pheromone system protein surrogates, and uses therefor
JOURNAL Patent: US 5789184-A 44 04-AUG-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR020656 (1-20)
Qy 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGATC 4
RESULT 214
LOCUS AR058897 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837836.
ACCESSION AR058897
VERSION AR058897.1 GI:5984474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Frederici,K., Jones,M.2., Chen,H. and Cavanagh,K.T.
TITLE Bovine beta.-mannosidase nucleic acid sequence
JOURNAL Patent: US 5837836-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR058897 (1-20)
Qy 179 IleLeuLeuProLeu 183
Db 6 ATTCTTTTACCCCTG 20
RESULT 215
LOCUS AR060887 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5840875.
ACCESSION AR060887
VERSION AR060887.1 GI:5987337
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Schreiner,G.F., Meyer,T.W. and Oberbauer,R.
TITLE Kidney Na/PO.sub.4 cotransporter antisense oligonucleotide
JOURNAL Patent: US 5840875-A 2 24-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR060887 (1-20)
Qy 102 ProAsnLeuSerLeu 106
Db 5 CCCAATCTCGCTG 19
RESULT 216
LOCUS AR061377 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 59 from patent US 5843653.
ACCESSION AR061377
VERSION AR061377.1 GI:5989068
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gold,L. and Tuerk,C.
TITLE Method for detecting a target molecule in a sample using a nucleic acid ligand
JOURNAL Patent: US 5843653-A 59 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR061377 (1-20)
Qy 32 ValValLysArgArg 36
Db 4 GTTGTAACACGACGG 18
RESULT 217
LOCUS AR067127/c 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 475 from patent US 5851760.
ACCESSION AR067127
VERSION AR067127.1 GI:5998349
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Evans,G.A. and Smith,M.W.

```

TITLE      Method for generation of sequence sampled maps of complex genomes
JOURNAL    Patent: US 5851760-A 475 22-DEC-1998;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR067127 (1-20)

QY      127 ArgArgLeuHisArg 131
       |||||
Db      18 AGAAGACTGCACAGA 4

RESULT 218
LOCUS   AR067298          20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 646 from patent US 5851760.
ACCESSION AR067298
VERSION   AR067298.1 GI:5998520
KEYWORDS "Unknown."
SOURCE   "Unknown."
ORGANISM "Unclassified."
REFERENCE 1 (bases 1 to 20)
AUTHORS   Evans, G.A. and Smith, M.W.
TITLE     Method for generation of sequence sampled maps of complex genomes
JOURNAL   Patent: US 5851760-A 646 22-DEC-1998;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR067298 (1-20)

QY      57 ValGluLeuLeuphe 61
       |||||
Db      18 GTTGAGCTGCTCTTC 4

RESULT 219
LOCUS   AR080740          20 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 45 from patent US 5968826.
ACCESSION AR080740
VERSION   AR080740.1 GI:10007470
KEYWORDS "Unknown."
SOURCE   "Unknown."
ORGANISM "Unclassified."
REFERENCE 1 (bases 1 to 20)
AUTHORS   Bennett, C. Frank, Condon, T.P. and Cowsett, L.M.
TITLE     Antisense inhibition of integrin .alpha.4 expression
JOURNAL   Patent: US 5968826-A 45 19-OCT-1999;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"

TITLE      Method for generation of sequence sampled maps of complex genomes
JOURNAL    Patent: US 5851760-A 475 22-DEC-1998;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR080740 (1-20)

QY      181 LeuProLeuTyrGlu 185
       |||||
Db      1 TTGCCCTTATATGAG 15

RESULT 220
LOCUS   AR085526          20 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION Sequence 4 from patent US 5981731.
ACCESSION AR085526
VERSION   AR085526.1 GI:10012293
KEYWORDS "Unknown."
SOURCE   "Unknown."
ORGANISM "Unclassified."
REFERENCE 1 (bases 1 to 20)
AUTHORS   Monia, B.P.
TITLE     Antisense oligonucleotide modulation of B-raf gene expression
JOURNAL   Patent: US 5981731-A 4 09-NOV-1999;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%         Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x AR085526 (1-20)

QY      169 SerValArgLeuSer 173
       |||||
Db      4 TCTGTAGGCTTCA 18

RESULT 221
LOCUS   AR099542          20 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 69 from patent US 6077833.
ACCESSION AR099542
VERSION   AR099542.1 GI:12809308
KEYWORDS "Unknown."
SOURCE   "Unknown."
ORGANISM "Unclassified."
REFERENCE 1 (bases 1 to 20)
AUTHORS   Bennett, C. Frank, and Vickers, T.A.
TITLE     Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
JOURNAL   Patent: US 6077833-A 69 20-JUN-2000;
FEATURES   Location/Qualifiers
           source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:

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Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR099542 (1-20)

QY 176 LeuArgArgileu 180
DB 1 CTGCGCGAATCCTG 15

RESULT 222
AR108276 LOCUS linear PAT 14-FEB-2001
DEFINITION Sequence 59 from patent US 6110900.
ACCESSION AR108276
VERSION AR108276.1 GI:12823763
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gold, L. and Tuerc, C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 6110900-A 59 29-AUG-2000;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR108276 (1-20)

QY 32 ValVallysArg 36
DB 4 GTTGTAACGACGG 18

RESULT 223
AR112948 LOCUS linear PAT 16-MAY-2001
DEFINITION Sequence 34 from patent US 6132724.
ACCESSION AR112948
VERSION AR112948.1 GI:14093270
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Blum, X.
TITLE Allelic polygene diagnosis of reward deficiency syndrome and treatment
JOURNAL Patent: US 6132724-A 34 17-OCT-2000;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR112948 (1-20)

QY 22 LysGlyArgArgGlu 26
DB 5 AAGGAGGAGGAA 19

RESULT 224
AR122465 LOCUS linear PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6165728.
ACCESSION AR122465
VERSION AR122465.1 GI:14106782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward, D.T. and Cowser, L.M.
TITLE Antisense modulation of NCK-2 expression
JOURNAL Patent: US 6165728-A 19 26-DEC-2000;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR122465 (1-20)

QY 163 GluGlyLeuHisGlu 167
DB 15 GAAGGACTCCATGAA 1

RESULT 225
AR122466 LOCUS linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6165728.
ACCESSION AR122466
VERSION AR122466.1 GI:14106783
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ward, D.T. and Cowser, L.M.
TITLE Antisense modulation of NCK-2 expression
JOURNAL Patent: US 6165728-A 20 26-DEC-2000;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR122466 (1-20)

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Qy 163 GluGlyLeuHisGlu 167
Db 20 GAAGGACTCCATGAA 6

RESULT 226
AR124504
LOCUS AR124504 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 73 from patent US 6171860.
ACCESSION AR124504
VERSION AR124504.1 GI:14109865
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of rank expression
JOURNAL Patent: US 6171860-A 73 09-JAN-2001;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 9.13e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x AR124504 (1-20)

Qy 128 ArgLeuHisArgAla 132
Db 2 AGGCTGCACCGGGCT 16

RESULT 227
AR130005
LOCUS AR130005 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6187585.
ACCESSION AR130005
VERSION AR130005.1 GI:14117902
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Lipton,A. and Witters,L.M.
TITLE Oligonucleotide inhibition of epidermal growth factor receptor
JOURNAL expression
FEATURES
source
Patent: US 6187585-A 7 13-FEB-2001;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 9.13e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x AR130005 (1-20)

Qy 129 LeuHisArgAlaGly 133
Db 6 TTGCACAGGCAGGG 20

RESULT 228
AR136419
LOCUS AR136419 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 14 from patent US 6136604.
ACCESSION AR136419
VERSION AR136419.1 GI:14477091
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Wyatt,J.
TITLE Antisense inhibition of methionine aminopeptidase 2 expression
JOURNAL Patent: US 6136604-A 14 24-OCT-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 9.13e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x AR136419 (1-20)

Qy 70 LeuAspProGlyArg 74
Db 6 CTGGATCCAGGTCGC 20

RESULT 229
AR136541/c
LOCUS AR136541 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 31 from patent US 6136952.
ACCESSION AR136541
VERSION AR136541.1 GI:14477213
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Li,L. and Hood,L.
TITLE Human jagged polypeptide, encoding nucleic acids and methods of use
JOURNAL Patent: US 6136952-A 31 24-OCT-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 9.13e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 6

US-09-966-880A-8 (1-198) x AR136541 (1-20)

Qy 27 ThrTyrLeuCysTyr 31
Db 16 ACATACCTCTGTAC 2

RESULT 230
AR137608/c
LOCUS AR137608 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 2 from patent US 6197532.
ACCESSION AR137608
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Paul, J. and Trueheart, J.
Methods for identifying G protein coupled receptor effectors
JOURNAL Patent: US 625059-A 49 03-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR160292 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 235
AR161622
LOCUS AR161622 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6255475.
ACCESSION AR161622
VERSION AR161622.1 GI:16227596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kwiatkowski, M.
TITLE Chain terminators, the use thereof for nucleic acid sequencing and synthesis and a method of their preparation
JOURNAL Patent: US 6255475-A 4 03-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR161622 (1-20)

QY 32 ValValLysArgArg 36
Db 5 GTTGTAAACGACGG 19

RESULT 236
AR162723
LOCUS AR162723 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 45 from patent US 6258790.
ACCESSION AR162723
VERSION AR162723.1 GI:16230060
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Condon, T. P. and Cowser, L. M.
TITLE Antisense modulation of integrin .alpha.4 expression
JOURNAL Patent: US 6258790-A 45 10-JUL-2001;
FEATURES Location/Qualifiers

Paul, J. and Trueheart, J.
Methods for identifying G protein coupled receptor effectors
JOURNAL Patent: US 625059-A 49 03-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR162723 (1-20)

QY 181 LeuProLeuTyrGlu 185
Db 1 TTGCCCTTATATGAG 15

RESULT 237
AR162748
LOCUS AR162748 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 71 from patent US 6258790.
ACCESSION AR162748
VERSION AR162748.1 GI:16230086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Condon, T. P. and Cowser, L. M.
TITLE Antisense modulation of integrin .alpha.4 expression
JOURNAL Patent: US 6258790-A 71 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR162748 (1-20)

QY 181 LeuProLeuTyrGlu 185
Db 4 TTGCCCTTATATGAG 18

RESULT 238
AR163037
LOCUS AR163037 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 20 from patent US 6270963.
ACCESSION AR163037
VERSION AR163037.1 GI:16233512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Stevens, J. K., Dunn, J. M., Capatos, D. and Matthews, D. E.
TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 6270963-A 20 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 243
LOCUS ARI170749 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 16 from patent US 6291741.
ACCESSION ARI170749
VERSION ARI170749.1 GI:17908708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul W., Scott, R.John., Betzner, A., Huttner, E., Lensee, P. and Perez, P.
TITLE Method for the production of modified plants
JOURNAL Patent: US 6291741-A 16 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI170749 (1-20)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 244
LOCUS ARI170751 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 18 from patent US 6291741.
ACCESSION ARI170751
VERSION ARI170751.1 GI:17908710
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Paul, W., Scott, R.John., Betzner, A., Huttner, E., Lensee, P. and Perez, P.
TITLE Method for the production of modified plants
JOURNAL Patent: US 6291741-A 18 18-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI170751 (1-20)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

Db 2 GTTGTAAACGACGG 16

RESULT 245
LOCUS ARI173022/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 147 from patent US 6303374.
ACCESSION ARI173022
VERSION ARI173022.1 GI:17912513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang, H. and Cowser, L.M.
TITLE Antisense modulation of caspase 3 expression
JOURNAL Patent: US 6303374-A 147 16-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI173022 (1-20)

Qy 41 SerPheSerLeuAsp 45
Db 15 TCCCTCTCCCTGGAC 1

RESULT 246
LOCUS ARI173845 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 43 from patent US 6306606.
ACCESSION ARI173845
VERSION ARI173845.1 GI:17914165
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weber, M.J., Wyatt, J. and Cowser, L.M.
TITLE Antisense modulation of MP-1 expression
JOURNAL Patent: US 6306606-A 43 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ARI173845 (1-20)

Qy 72 ProGlyArgCysTyr 76
Db 2 CCTGTAGCTGTAT 16

RESULT 247
LOCUS ARI178823 20 bp DNA linear PAT 20-APR-2002

```
DEFINITION Sequence 69 from patent US 6319906.
ACCESSION AR178823
VERSION AR178823.1 GI:20219961
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
JOURNAL expression of B7 protein
PATENT: US 6319906-A 69 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR178823 (1-20)
QY 176 LeuArgArgIleLeu 180
|||||
Db 1 CTGCGCGAATCCTG 15

RESULT 248
AR178920
LOCUS AR178920 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 166 from patent US 6319906.
ACCESSION AR178920
VERSION AR178920.1 GI:20220058
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE Unclassified.
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
JOURNAL expression of B7 protein
PATENT: US 6319906-A 166 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR178920 (1-20)
QY 176 LeuArgArgIleLeu 180
|||||
Db 2 CTGCGCGAATCCTG 16

RESULT 249
BD227783
LOCUS BD227783 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of integrin alph 4 expression.
ACCESSION BD227783
VERSION BD227783.1 GI:33037553

KEYWORDS JP 2002526555-A/45.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Condon,T.P. and Cowsett,L.M.
TITLE Antisense modulation of integrin alph 4 expression
JOURNAL Patent: JP 2002526555-A 45 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526555-A/45
PD 20-AUG-2002
PF 19-AUG-1999 JP 2000574727
PR 05-OCT-1998 US 09/166203
PI FRANK C BENNETT,THOMAS P CONDON,LEX M COWSETT PC
C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
00,A61P1/16,
PC A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P35/00, PC
A61P35/04,
PC A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
antisense sequence
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x BD227783 (1-20)
QY 181 LeuProLeuTyGlu 185
|||||
Db 1 TTGCCCTTATAG 15

RESULT 250
BD230169/c
LOCUS BD230169 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230169
VERSION BD230169.1 GI:33039939
KEYWORDS JP 2002530091-A/38.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 20)
AUTHORS Galibert,F. and Andre,C.
TITLE Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes
JOURNAL Patent: JP 2002530091-A 38 17-SEP-2002;
COMMENT CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/38
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT,CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC Ren04F08
FH Key Location/Qualifiers
FT source 1..20
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FT /organism='Canis familiaris (dog)'

FEATURES
source

Location/Qualifiers
1..20
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x BD230169 (1-20)

QY 129 LeuHisArgAlaGly 133
DB 20 CTCACAGGCGAGG 6

RESULT 251
BD237751/c
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Human proteins participating in protein decomposition of
endoplasmic reticulum.

ACCESSION BD237751
VERSION BD237751.1 GI:33047521
KEYWORDS JP 2002527111-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 20)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Chau V.

TITLE Human proteins participating in protein decomposition of

endoplasmic reticulum

JOURNAL Patent: JP 2002527111-A 5 27-AUG-2002;

COMMENT MILLENNIUM PHARMACEUTICALS INC

OS Homo sapiens (human)
PN JP 2002527111-A/5
PD 27-AUG-2002

PF 21-OCT-1999 JP 2000577306
PR 21-OCT-1998 US 60/105064
PI VINCENT CHAU

PC C12N15/09,A61K31/7105,A61K45/00,A61K48/00,A61P1/16,A61P11/00,
PC A61P35/00,C12N9/00,C12Q1/02,C12Q1/68,C12N15/00 CC Human

PC C07K14/47,C12N9/00,C12Q1/02,C12Q1/68,C12N15/00 CC Human
proteins participating in protein decomposition of CC
endoplasmic

CC reticulum

FT Key Location/Qualifiers
FT source 1..20 /organism='Homo sapiens (human)'

FT Location/Qualifiers

1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x BD237751 (1-20)

QY 130 HisArgAlaGlyVal 134

Db 17 CATCGCGAGGAGTG 3

RESULT 252

E07640

LOCUS

DEFINITION

Olignonucleotide.

ACCESSION E07640

VERSION E07640.1 GI:2175775

KEYWORDS JP 1994153997-A/1.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Okamoto,H., Yamamoto,N., Tomita,Y., Kawaguchi,M., Murakami,A. and

Makino,K.

TITLE METHOD FOR DETECTING TARGET NUCLEIC ACID BY AMPLIFICATION OF

DETECTED SIGNAL

JOURNAL Patent: JP 1994153997-A 1 03-JUN-1994;

COMMENT CANON INC

OS None

CC Artificial sequences.

PN JP 1994153997-A/1

PD 03-JUN-1994

PF 27-NOV-1992 JP 1992318958

PI OKAMOTO HISASHI, YAMAMOTO NOBUKO, TOMITA YOSHINORI, PI

KAWAGUCHI MASAHIRO,

PI MURAKAMI AKIRA, MAKINO KEISUKE

PC C12Q1/68,C07H21/04,G01N24/00,G01N33/58//A61B10/00; CC

strandedness: Single;

CC topology: Linear;

FT Key Location/Qualifiers

FT source 1..20

FT Location/Qualifiers

1..20 /organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 9.13e+03 Length: 20

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: Gaps: 0

US-09-966-880A-8 (1-198) x E07640 (1-20)

QY 32 ValVallyArgArg 36

DB 1 GTTGTAACGACGG 15

RESULT 253

E07641

LOCUS

DEFINITION

Olignonucleotide.

ACCESSION E07641

VERSION E07641.1 GI:2175776

KEYWORDS JP 1994153998-A/1.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y., Makino,K. and

Murakami,A.

TITLE METHOD FOR DETECTING NUCLEIC ACID HYBRID BODY AND PROBE USED

JOURNAL Patent: JP 1994153998-A 1 03-JUN-1994;

COMMENT CANON INC

OS None

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OC Artificial sequences.
PN JP 1994153998-A/1
PD 03-JUN-1994
PF 27-NOV-1992 JP 1992318959
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASASHIRO, PI
TOMITA YOSHINORI,
PI MAKINO KEISUKE, MURAKAMI AKIRA
PC C12Q1/68,C07H21/04,G01N24/00,G01N33/58//A61B10/00; CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/db_xref="taxon:32644"
/organism="Artificial sequences".

FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x E07641 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 254
E07642
LOCUS E07642 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide.
ACCESSION E07642
VERSION E07642.1 GI:2175777
KEYWORDS JP 1994153999-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y., Makino,K. and
Murakami,A.
TITLE METHOD FOR DETECTING TARGET NUCLEIC ACID USING CHARGE TRANSFER TYPE
PIGMENT AND PROBE USED THEREFOR
JOURNAL Patent: JP 1994153999-A 1 03-JUN-1994;
CANON INC
COMMENT OS None
OC Artificial sequences.
PN JP 1994153999-A/1
PD 03-JUN-1994
PF 30-NOV-1992 JP 1992320500
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASASHIRO, PI
TOMITA YOSHINORI,
PI MAKINO KEISUKE, MURAKAMI AKIRA
PC C12Q1/68,C07H21/04,G01N21/17,G01N24/00,G01N33/58//A61B10/00;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/db_xref="taxon:32644"
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

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Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x E07642 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 255
E10364
LOCUS E10364 20 bp DNA linear PAT 29-SEP-1997
DEFINITION M13mpl8DNA probe.
ACCESSION E10364
VERSION E10364.1 GI:22027193
KEYWORDS JP 1995313199-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N. and Okamoto,H.
TITLE DETECTION OF TARGET SUBSTANCE IN SPECIMEN
JOURNAL Patent: JP 1995313199-A 1 05-DEC-1995;
CANON INC
COMMENT OS None
OC Artificial sequences.
PN JP 1995313199-A/1
PD 05-DEC-1995
PF 26-MAY-1994 JP 1994112626
PI YAMAMOTO NOBUKO, OKAMOTO HISASHI
PC C12Q1/68,G01N33/58//C07D309/34,C07D335/02,C07D409/04, PC
C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/db_xref="taxon:32644"
/organism="Artificial sequences".

FEATURES
source Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x E10364 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 256
E12624
LOCUS E12624 20 bp DNA linear PAT 27-APR-1998
DEFINITION DNA probe.
ACCESSION E12624
VERSION E12624.1 GI:3251456
KEYWORDS JP 1997040661-A/1.
SOURCE unidentified

```

```

ORGANISM      unidentified
unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Yamamoto,N., Okamoto,H., Kawaguchi,M., Tomita,Y. and Miyazaki,I.
TITLE          FLUORESCENT DYE CONTAINING PYRYLIUM SALT OR PYRYLIUM ANALOGOUS
               SALT, AND DETECTION OF NUCLEIC ACID AND FLUORESCENT DYEING OF
               ORGANISM SPECIMEN USING THE SAME
JOURNAL        Patent: JP 1997040661-A 1 10-FEB-1997;
               CANON INC
COMMENT        OS None
               OC Artificial sequences.
               PN JP 1997040661-A/1
               PD 10-FEB-1997
               PF 17-DEC-1993 JP 1996200327
               PR 21-DEC-1992 JP 92P 340755, 10-MAR-1993 JP 93P 49530, PR
               13-SEP-1993 JP 93P 227204, 26-OCT-1993 JP 93P 266866 PI
               YAMAMOTO NOBUKO, OKAMOTO HISASHI, KAWAGUCHI MASAHIRO, PI
               YOSHINORI,
               PI MIYAZAKI TAKESHI
               PC C07D309/34;C07D335/02,C07D345/00,C09K11/06,C12Q1/68,G01N21/78,
               PC G01N27/447,
               PC G01N33/50//C07D407/14,C07D409/08,C07D409/14,C12N15/09; CC
               strandedness: single;
               CC Topology: Linear;
               FH Key      Location/Qualifiers
               FH source   1..20
               FT source   /organism='Artificial sequences'.
FEATURES      source
               Location/Qualifiers
               1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:        0
US-09-966-880A-8 (1-198) x E25557 (1-20)
QY      32 ValVallysArgArg 36
Db      1 GTTGTAACGACGG 15
RESULT 258
E25557
LOCUS      20 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for detecting target nucleic acid.
ACCESSION  E25557
VERSION     E25557.1 GI:13024829
KEYWORDS   JP 1999127897-A/1.
SOURCE     unidentified
           ORGANISM
           unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE      Method for detecting target nucleic acid
JOURNAL    Patent: JP 1999127897-A 1 18-MAY-1999;
           CANON INC
COMMENT    OS Unidentified
           PN JP 1999127897-A/1
           PD 18-MAY-1999
           PF 31-OCT-1997 JP 1997300944
           PR
           PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
           MITSUHIKO SHIOYA
           PC C12Q1/68//C12N15/09,C12N15/00
           CC Topology: Linear;
           FH Key      Location/Qualifiers
           FH source   1..20
           FT source   /organism='Unidentified'.
FEATURES      source
               Location/Qualifiers
               1..20
               /organism='unidentified'
               /mol_type='genomic DNA'
               /db_xref='taxon:32644'
ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%        Indels:      0
DB:             6           Gaps:        0
US-09-966-880A-8 (1-198) x E25557 (1-20)
QY      32 ValVallysArgArg 36
Db      1 GTTGTAACGACGG 15
RESULT 257
E25557
LOCUS      20 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for detecting target nucleic acid.
ACCESSION  E25557
VERSION     E25557.1 GI:13024823
KEYWORDS   JP 1999127862-A/1.
SOURCE     unidentified
           ORGANISM
           unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE      Method for detecting target nucleic acid
JOURNAL    Patent: JP 1999127862-A 1 18-MAY-1999;
           CANON INC
COMMENT    OS Unidentified
           PN JP 1999127862-A/1
           PD 18-MAY-1999
           PF 31-OCT-1997 JP 1997300943
           PR
           PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
           MITSUHIKO SHIOYA
           PC C12N15/09,C12Q1/68,C12N15/00
           CC Topology: Linear;

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E25564/c
LOCUS          E25564          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25564
VERSION        E25564.1  GI:13024830
KEYWORDS       JP 1999127897-A/2.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE         Method for detecting target nucleic acid
JOURNAL       Patent: JP 1999127897-A 2 18-MAY-1999;
              CANON INC
COMMENT       OS Unidentified
              PN JP 1999127897-A/2
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              CC C12Q1/68//C12N15/09,C12N15/00
              FH Key
              FT source
              FT Location/Qualifiers
              FT /organism='Unidentified'.
              FT 1..20
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25564 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25568          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25568
VERSION        E25568.1  GI:13024834
KEYWORDS       JP 1999127897-A/6.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE         Method for detecting target nucleic acid
JOURNAL       Patent: JP 1999127897-A 6 18-MAY-1999;
              CANON INC
COMMENT       OS Unidentified
              PN JP 1999127897-A/6
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              CC C12Q1/68//C12N15/09,C12N15/00
              FH Key
              FT source
              FT Location/Qualifiers
              FT /organism='Unidentified'.
              FT 1..20
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25564 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25567/c          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25567
VERSION        E25567.1  GI:13024833
KEYWORDS       JP 1999127897-A/5.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE         Method for detecting target nucleic acid
JOURNAL       Patent: JP 1999127897-A 5 18-MAY-1999;
              CANON INC
COMMENT       OS Unidentified
              PN JP 1999127897-A/5
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              CC C12Q1/68//C12N15/09,C12N15/00
              FH Key
              FT source
              FT Location/Qualifiers
              FT /organism='Unidentified'.
              FT 1..20
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 260
LOCUS          E25567/c          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25567
VERSION        E25567.1  GI:13024833
KEYWORDS       JP 1999127897-A/5.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE         Method for detecting target nucleic acid
JOURNAL       Patent: JP 1999127897-A 5 18-MAY-1999;
              CANON INC
COMMENT       OS Unidentified
              PN JP 1999127897-A/5
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              CC C12Q1/68//C12N15/09,C12N15/00
              FH Key
              FT source
              FT Location/Qualifiers
              FT /organism='Unidentified'.
              FT 1..20
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 262
LOCUS          E36214          20 bp      DNA          linear          PAT 31-JAN-2002

```

```

FEATURES
source
Location/Qualifiers
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25567 (1-20)

Qy 32 ValVallysArgArg 36
Db 20 GTTGTAAACGACGG 6

RESULT 261
LOCUS          E25568          20 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for detecting target nucleic acid.
ACCESSION      E25568
VERSION        E25568.1  GI:13024834
KEYWORDS       JP 1999127897-A/6.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Tomohiro,S., Hisashi,O., Nobuko,Y. and Mitsuhiro,S.
TITLE         Method for detecting target nucleic acid
JOURNAL       Patent: JP 1999127897-A 6 18-MAY-1999;
              CANON INC
COMMENT       OS Unidentified
              PN JP 1999127897-A/6
              PD 18-MAY-1999
              PF 31-OCT-1997 JP 1997300944
              PR
              PI TOMOHIRO SUZUKI,HISASHI OKAMOTO,NOBUKO YAMAMOTO, PI
              MITSUHIKO SHIOYA
              CC C12Q1/68//C12N15/09,C12N15/00
              FH Key
              FT source
              FT Location/Qualifiers
              FT /organism='Unidentified'.
              FT 1..20
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:     5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%        Indels:      0
DB:             6            Gaps:        0

US-09-966-880A-8 (1-198) x E25568 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 262
LOCUS          E36214          20 bp      DNA          linear          PAT 31-JAN-2002

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DEFINITION Japanese citrus viroid 1 (JCVd1) gene.
ACCESSION E36214
VERSION E36214.1 GI:18626426
KEYWORDS JP 2000166566-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ito,T., Yashiro,H. and Ozaki,K.
TITLE Japanese citrus viroid 1 (JCVd1) gene
JOURNAL FRUIT TREE RES STATION
COMMENT OS Artificial Sequence
PN JP 2000166566-A/6
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349471
PR
PI TAKAO ITO,HIROYUKI YASHIRO,KATSUMI OZAKI
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/mol_type='synthetic construct'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E59388 (1-20)
QY 40 ThrSerPheSerLeu 44
DB 1 ACCTCGTTTAGTTTG 15
RESULT 264
E64279
LOCUS E64279 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Polynucleotide molecule encoding Neospora protein.
ACCESSION E64279
VERSION E64279.1 GI:13017785
KEYWORDS JP 1999332583-A/11.
SOURCE Neospora caninum
ORGANISM Neospora caninum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Neospora.
REFERENCE 1 (bases 1 to 20)
AUTHORS David,A.B., Rebecca,A.M., Bekki,A.D., Barakurishunan,R.K. and
Susan,C.Y.
TITLE Polynucleotide molecule encoding Neospora protein
JOURNAL Patent: JP 1999332583-A 11 07-DEC-1999;
PFIZER PROD INC
COMMENT OS Neospora caninum
PN JP 1999332583-A/11
PD 07-DEC-1999
PF 25-MAR-1999 JP 1999081833
PR 26-MAR-1998 US 60/079389,15-DEC-1998 US 60/112282 PI
DAVID ALLAN BLAKE,REBECCA ANNE MADURA,BEKKI ANNE DATSUKI, PI
BARAKURISHUNAN RAJENDORA KRISHNAN,SUSAN CHRISTINE YODA PC
C12N15/09,A61K31/00,A61K35/12,A61K38/00,A61K39/39,C07K14/44, PC
C07K16/18,
PC C12N15/02,C12P21/02,C12P21/08,C12N15/00,A61K37/02,C12N15/00 CC
FEATURES
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Neospora caninum'.
FEATURES
source Location/Qualifiers
1..20
/mol_type='genomic DNA'
/db_xref='taxon:29176'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E64279 (1-20)
QY 39 AlaThrSerPheSer 43
DB 4 GCGACTCTCTTTTCT 18
DEFINITION Japanese citrus viroid 1 (JCVd1) gene.
ACCESSION E36214
VERSION E36214.1 GI:18626426
KEYWORDS JP 2000166566-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ito,T., Yashiro,H. and Ozaki,K.
TITLE Japanese citrus viroid 1 (JCVd1) gene
JOURNAL FRUIT TREE RES STATION
COMMENT OS Artificial Sequence
PN JP 2000166566-A/6
PD 20-JUN-2000
PF 09-DEC-1998 JP 1998349471
PR
PI TAKAO ITO,HIROYUKI YASHIRO,KATSUMI OZAKI
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..20
/mol_type='synthetic construct'
/db_xref='taxon:32630'
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x E36214 (1-20)
QY 97 PheLeuArgGlyAsn 101
DB 5 TTCTCTCGGGGAAC 19
RESULT 263
E59388
LOCUS E59388 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for differentiating varieties of pig by DNA sequence
polymorphism.
ACCESSION E59388
VERSION E59388.1 GI:18622523
KEYWORDS JP 200030586-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mitsuhashi,T. and Okumura,N.
TITLE Method for differentiating varieties of pig by DNA sequence
JOURNAL Patent: JP 200030586-A 12 19-DEC-2000;
LINESSTOCK EXPERIMENT STATION MINISTRY OF AGRICULTURE FORESTRY AND
FISHERIES, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY
AND FISHERIES, TADAYOSHI MITSUHASHI
OS Artificial Sequence
PN JP 200030586-A/12
PD 19-DEC-2000
PF 11-JUN-1999 JP 1999165269
PR
PI TADAYOSHI MITSUHASHI,NAOHIKO OKUMURA
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.

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RESULT 265
I16233
LOCUS I16233 20 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 59 from patent US 5475096.
ACCESSION I16233
VERSION I16233.1 GI:1251141
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gold,L. and Tuerk,C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5475096-A 59 12-DEC-1995;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I16233 (1-20)
QY 32 ValValLysArgArg 36
DB 4 GTTGTAACGACGG 18
RESULT 266
I23911/c
LOCUS I23911 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 13 from patent US 5541060.
ACCESSION I23911
VERSION I23911.1 GI:1603781
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bell,G.I., Stoffel,M., Takeda,J., Vionnet,N., Yasuda,K.,
Pikis,S.J., Zouali,H., Velho,G., Cohen,D. and Froguel,P.
TITLE Detection of glucokinase-linked early-onset non-insulin-dependent
diabetes mellitus
JOURNAL Patent: US 5541060-A 13 30-JUL-1996;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I23911 (1-20)
QY 104 LeuSerLeuArgIle 108
DB 18 TTGAGCCTCAGATC 4
RESULT 267
I24636
LOCUS I24636 20 bp DNA linear PAT 07-OCT-1996

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DEFINITION Sequence 20 from patent US 5545527.
ACCESSION I24636
VERSION I24636.1 GI:1604506
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Stevens,J.K. and Dunn,J.M.
TITLE Method for testing for mutations in DNA from a patient sample
JOURNAL Patent: US 5545527-A 20 13-AUG-1996;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I24636 (1-20)
QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTTATGTT 16
RESULT 268
I25233
LOCUS I25233 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 20 from patent US 5550020.
ACCESSION I25233
VERSION I25233.1 GI:1605103
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gallie,B.L., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for
retinoblastoma
JOURNAL Patent: US 5550020-A 20 27-AUG-1996;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I25233 (1-20)
QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTTATGTT 16
RESULT 269
I31646
LOCUS I31646 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 47 from patent US 5582983.
ACCESSION I31646
VERSION I31646.1 GI:1822437
KEYWORDS

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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,D.M. and Scholin,C.A.
TITLE Genetic markers and methods of identifying alexandrium
(dinophyceae) species
JOURNAL Patent: US 5582983-A 47 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I31646 (1-20)
Qy 170 ValArgLeuSerArg 174
Db 6 GTCGCTCTTCAAGA 20
RESULT 270
I36171/c 20 bp DNA linear PAT 13-MAY-1997
LOCUS
DEFINITION Sequence 7 from patent US 5605662.
ACCESSION I36171
VERSION I36171.1 GI:2086684
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heller,M.J. and Tu,B.
TITLE Active programmable electronic devices for molecular biological
analysis and diagnostics
JOURNAL Patent: US 5605662-A 7 25-FEB-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I36171 (1-20)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4
RESULT 271
I36258
LOCUS
DEFINITION Sequence 3 from patent US 5605797.
ACCESSION I36258
VERSION I36258.1 GI:2086771
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.
TITLE Bovine .beta.-mannosidase gene and methods of use
JOURNAL Patent: US 5605797-A 3 25-FEB-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I36258 (1-20)
Qy 179 IleLeuLeuProLeu 183
Db 6 ATTCCTTTACCCCTG 20
RESULT 272
I41050
LOCUS
DEFINITION Sequence 1 from patent US 5624798.
ACCESSION I41050
VERSION I41050.1 GI:2081640
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yamamoto,N., Okamoto,T., Tomida,Y., Miyazaki,T. and Kawaguchi,M.
TITLE Detection method of nucleic acid by use of fluorescent pyrylium
stain in intercalation into nucleic acids
JOURNAL Patent: US 5624798-A 1 29-APR-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x I41050 (1-20)
Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15
RESULT 273
I66719
LOCUS
DEFINITION Sequence 59 from patent US 5670637.
ACCESSION I66719
VERSION I66719.1 GI:2724697
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gold,L. and Tuerk,C.
TITLE Nucleic acid ligands
JOURNAL Patent: US 5670637-A 59 23-SEP-1997;

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FEATURES
source      Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I66719 (1-20)

Qy 32 ValVallysArgArg 36
Db 4 GTTGTAAACGACGG 18

RESULT 274
LOCUS      I70204      20 bp      DNA      linear      PAT 02-APR-1998
DEFINITION Sequence 1 from patent US 5679516.
ACCESSION  I70204
VERSION    I70204.1 GI:3006339
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Okamoto,T. and Miyazaki,T.
TITLE     Process for detecting nucleic acid by capillary electrophoresis
JOURNAL   Patent: US 5679516-A 1 21-OCT-1997;
FEATURES   Location/Qualifiers
source    1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I70204 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 275
I70205/c
LOCUS      I70205      20 bp      DNA      linear      PAT 02-APR-1998
DEFINITION Sequence 2 from patent US 5679516.
ACCESSION  I70205
VERSION    I70205.1 GI:3006340
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Okamoto,T. and Miyazaki,T.
TITLE     Process for detecting nucleic acid by capillary electrophoresis
JOURNAL   Patent: US 5679516-A 2 21-OCT-1997;
FEATURES   Location/Qualifiers
source    1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I70204 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 276
LOCUS      I84265      20 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 36 from patent US 5695926.
ACCESSION  I84265
VERSION    I84265.1 GI:3021785
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Cros,P., Allibert,P., Mallet,F., Mabilat,C. and Mandrand,B.
TITLE     Sandwich hybridization assays using very short capture probes
JOURNAL   Patent: US 5695926-A 36 09-DEC-1997;
FEATURES   Location/Qualifiers
source    1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I84265 (1-20)

Qy 174 ArgGlnLeuArgArg 178
Db 1 AGACAGCTCAGAGA 15

RESULT 277
LOCUS      I84813      20 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 59 from patent US 5696249.
ACCESSION  I84813
VERSION    I84813.1 GI:3022333
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Gold,L. and Tuerk,C.
TITLE     Nucleic acid ligands
JOURNAL   Patent: US 5696249-A 59 09-DEC-1997;
FEATURES   Location/Qualifiers
source    1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I84813 (1-20)

Qy 174 ArgGlnLeuArgArg 178
Db 1 AGACAGCTCAGAGA 15

RESULT 277
LOCUS      I84813      20 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 59 from patent US 5696249.
ACCESSION  I84813
VERSION    I84813.1 GI:3022333
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Gold,L. and Tuerk,C.
TITLE     Nucleic acid ligands
JOURNAL   Patent: US 5696249-A 59 09-DEC-1997;
FEATURES   Location/Qualifiers
source    1..20
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      9.13e+03      Length:      20
Score:          5.00          Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Query Match:    2.53%          Indels:      0
DB:            6              Gaps:        0

US-09-966-880A-8 (1-198) x I84813 (1-20)

Qy 174 ArgGlnLeuArgArg 178
Db 1 AGACAGCTCAGAGA 15
```

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 6
Gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0

US-09-966-880A-8 (1-198) x I84813 (1-20)

QY 32 ValVallysargarg 36
DB 4 GTTGTAAACGACGG 18

RESULT 278

AR180892 AR180892 20 bp DNA linear PAT 20-APR-2002

LOCUS AR180892 Sequence 67 from patent US 6333158.

DEFINITION AR180892

ACCESSION AR180892

VERSION AR180892.1 GI:20222925

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Uemori, T., Sato, Y., Fujita, T., Miyake, K., Mukai, H., Asada, K. and

Kato, I.

TITLE DNA polymerase-related factors

JOURNAL Patent: US 6333158-A 67 25-DEC-2001;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 6
Gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0

US-09-966-880A-8 (1-198) x AR180892 (1-20)

QY 156 GluArgThrPheLys 160
DB 3 GAGAGACTTTCAG 17

RESULT 279

AR216046 AR216046 20 bp DNA linear PAT 25-SEP-2002

LOCUS AR216046 Sequence 93 from patent US 6410518.

DEFINITION AR216046

ACCESSION AR216046

VERSION AR216046.1 GI:23314334

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Monia, B.P.

TITLE Antisense oligonucleotide inhibition of raf gene expression

JOURNAL Patent: US 6410518-A 93 25-JUN-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 6
Gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0

US-09-966-880A-8 (1-198) x AR216046 (1-20)

QY 169 SerValArgLeuSer 173
DB 4 TCTGTAAAGGCTTCA 18

RESULT 280

AR224743 AR224743 20 bp DNA linear PAT 26-SEP-2002

LOCUS AR224743 Sequence 48 from patent US 6440739.

DEFINITION AR224743

ACCESSION AR224743

VERSION AR224743.1 GI:23333583

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett, C.F. and Freier, S.M.

TITLE Antisense modulation of glioma-associated oncogene-2 expression

JOURNAL Patent: US 6440739-A 48 27-AUG-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 6
Gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0

US-09-966-880A-8 (1-198) x AR224743 (1-20)

QY 130 HisArgAlaGlyVal 134
DB 20 CACCGGCGAGGTGTA 6

RESULT 281

AR225942 AR225942 20 bp DNA linear PAT 20-DEC-2002

LOCUS AR225942 Sequence 5 from patent US 6444465.

DEFINITION AR225942

ACCESSION AR225942

VERSION AR225942.1 GI:27264096

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wyatt, J. and Freier, S.M.

TITLE Antisense modulation of Her-1 expression

JOURNAL Patent: US 6444465-A 5 03-SEP-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
DB: 6
Gaps: 0
Conservative: 0
Mismatch: 0
Indels: 0

US-09-966-880A-8 (1-198) x AR225942 (1-20)

QY 129 LeuHisArgAlaGly 133
DB 129 LeuHisArgAlaGly 133

Db 6 TTGCACAGGCGAGGG 20
RESULT 282
AR229992
LOCUS 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 35 from patent US 6451538.
ACCESSION AR229992
VERSION AR229992.1 GI:27269884
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cowser,L.M.
TITLE Antisense modulation of CHK2 expression
JOURNAL Patent: US 6451538-A 35 17-SEP-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR229992 (1-20)
QY 110 ThrAlaArgLeuTyr 114
|||||
Db 4 ACAGCAGCGTTATAC 18
RESULT 283
AR232363
LOCUS 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 58 from patent US 6455308.
ACCESSION AR232363
VERSION AR232363.1 GI:27274355
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Freier,S.M.
TITLE Antisense modulation of serum amyloid A4 expression
JOURNAL Patent: US 6455308-A 58 24-SEP-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR232363 (1-20)
QY 42 PheSerLeuAspPhe 46
|||||
Db 3 TTCGTTGGACTTC 17
RESULT 284
AR234630/c
LOCUS 20 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 71 from patent US 6458591.
ACCESSION AR234630
VERSION AR234630.1 GI:27277337
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J.
TITLE Antisense modulation of phosphorylase kinase Alpha 2 expression
JOURNAL Patent: US 6458591-A 71 01-OCT-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR234630 (1-20)
QY 38 SerAlaThrSerPhe 42
|||||
Db 15 TCTGCCACTTCTTTT 1
RESULT 285
AR255289
LOCUS 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 56 from patent US 6482592.
ACCESSION AR255289
VERSION AR255289.1 GI:27304338
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using modular oligonucleotides
JOURNAL Patent: US 6482592-A 56 19-NOV-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR255289 (1-20)
QY 32 ValVallyeArgArg 36
|||||
Db 2 GTTGTAAACGACGG 16
RESULT 286
AR263237
LOCUS 20 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 59 from patent US 6331398.
ACCESSION AR263237
VERSION AR263237.1 GI:28074982
KEYWORDS

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR312669 (1-20)

QY 169 SerValArgLeuSer 173
|||||
Db 19 TCGGTGAGACTGTCT 5

RESULT 289
AR313167/c
LOCUS AR313167 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3704 from patent US 6559294.
ACCESSION AR313167
VERSION AR313167.1 GI:31706593
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 3704 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR313167 (1-20)

QY 103 AsnLeuSerLeuArg 107
|||||
Db 20 AACCTCTCTGTGAGG 6

RESULT 290
AR313194/c
LOCUS AR313194 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3731 from patent US 6559294.
ACCESSION AR313194
VERSION AR313194.1 GI:31706620
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 3731 06-MAY-2003;

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3206 from patent US 6559294.
ACCESSION AR312669
VERSION AR312669.1 GI:31706095
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseith,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.

Sankaran,B. and Fletcher,L.D.
Chlamydia pneumoniae polynucleotides and uses thereof
Patent: US 6559294-A 3206 06-MAY-2003;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AR272008 (1-20)

QY 44 LeuAspPheGlyTyr 48
|||||
Db 17 CTGGACTTTGGGTAT 3

RESULT 288
AR312669/c
LOCUS AR312669 20 bp DNA linear PAT 12-JUN-2003
DEF

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FEATURES             Location/Qualifiers
     source            1..20
                        /organism="unknown"
                        /mol_type="genomic DNA"

ORIGIN
Alignment Scores:      Length: 20
Pred. No.:             Matches: 5
Score:                 Conservative: 0
Percent Similarity:    100.00%
Best Local Similarity: 100.00%
Query Match:           Mismatches: 0
                        Indels: 0
                        Gaps: 0
DB:

US-09-966-880A-8 (1-198) x AR313194 (1-20)

QY      104 LeuSerLeuArgile 108
        16 TTGTCCTGAGAAATC 2

Db

RESULT 291
AR313438
LOCUS      AR313438                20 bp    DNA
DEFINITION Sequence 3975 from patent US 6559294.
ACCESSION AR313438
VERSION    AR313438.1 GI:31706864
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais,R., Hoiseeth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 3975 06-MAY-2003;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:      Length: 20
Pred. No.:             Matches: 5
Score:                 Conservative: 0
Percent Similarity:    100.00%
Best Local Similarity: 100.00%
Query Match:           Mismatches: 0
                        Indels: 0
                        Gaps: 0
DB:

US-09-966-880A-8 (1-198) x AR313438 (1-20)

QY      176 LeuArgArgileLeu 180
        6 TTGAGGAGGATCCTG 20

Db

RESULT 292
AR314006
LOCUS      AR314006                20 bp    DNA
DEFINITION Sequence 4543 from patent US 6559294.
ACCESSION AR314006
VERSION    AR314006.1 GI:31707432
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais,R., Hoiseeth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 4543 06-MAY-2003;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

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/mol_type="genomic DNA"

ORIGIN
Alignment Scores:      Length: 20
Pred. No.:             Matches: 5
Score:                 Conservative: 0
Percent Similarity:    100.00%
Best Local Similarity: 100.00%
Query Match:           Mismatches: 0
                        Indels: 0
                        Gaps: 0
DB:

US-09-966-880A-8 (1-198) x AR314006 (1-20)

QY      111 AlaArgLeuTyPhe 115
        2 GCCAGGCTGTATTC 16

Db

RESULT 293
AR314095
LOCUS      AR314095                20 bp    DNA
DEFINITION Sequence 4632 from patent US 6559294.
ACCESSION AR314095
VERSION    AR314095.1 GI:31707521
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais,R., Hoiseeth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 4632 06-MAY-2003;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:      Length: 20
Pred. No.:             Matches: 5
Score:                 Conservative: 0
Percent Similarity:    100.00%
Best Local Similarity: 100.00%
Query Match:           Mismatches: 0
                        Indels: 0
                        Gaps: 0
DB:

US-09-966-880A-8 (1-198) x AR314095 (1-20)

QY      179 IleLeuLeuProleu 183
        20 ATTCTACTCCCTCTC 6

Db

RESULT 294
AR314123/c
LOCUS      AR314123                20 bp    DNA
DEFINITION Sequence 4660 from patent US 6559294.
ACCESSION AR314123
VERSION    AR314123.1 GI:31707549
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Griffais,R., Hoiseeth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE      Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL    Patent: US 6559294-A 4660 06-MAY-2003;
FEATURES   Location/Qualifiers
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN

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Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR314123 (1-20)

QY 40 ThrSerPheSerLeu 44
DB 18 ACATCGTCTCCCTA 4

RESULT 295
LOCUS AR314875 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5412 from patent US 6559294.
ACCESSION AR314875
VERSION AR314875.1 GI:31708301
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5412 06-MAY-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR314875 (1-20)

QY 126 LeuArgArgLeuHis 130
DB 17 CTAAGGCGCTTACAT 3

RESULT 296
LOCUS AR315172 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5709 from patent US 6559294.
ACCESSION AR315172
VERSION AR315172.1 GI:31708598
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5709 06-MAY-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR315172 (1-20)

QY 104 LeuSerLeuArgIle 108
DB 15 CTGTCCTCCGCATA 1

RESULT 297
LOCUS AR315845 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6382 from patent US 6559294.
ACCESSION AR315845
VERSION AR315845.1 GI:31709271
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6382 06-MAY-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AR315845 (1-20)

QY 58 GluLeuLeuPheLeu 62
DB 20 GAGCTTCCTTTTAA 6

RESULT 298
LOCUS AR315964 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6501 from patent US 6559294.
ACCESSION AR315964
VERSION AR315964.1 GI:31709390
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6501 06-MAY-2003;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
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DB:
US-09-966-880A-8 (1-198) x AR315964 (1-20)
QY 41 SerPheSerLeuasp 45
Db 5 AGTTTCTCTAGAC 19

RESULT 299
AR336993
LOCUS AR336993 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 54 from patent US 6566132.
ACCESSION AR336993
VERSION AR336993.1 GI:33722847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watt,A.T.
TITLE Antisense modulation of Interferon gamma receptor 1 expression
JOURNAL Patent: US 6566132-A 54 20-MAY-2003;
FEATURES
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        location/Qualifiers
            1..20
                /organism="unknown"
                /mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR336993 (1-20)
QY 167 GluAsnSerValArg 171
Db 5 GAGAAATTCAGTGAGG 19

RESULT 300
AR350293/c
LOCUS AR350293 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 70 from patent US 6586245.
ACCESSION AR350293
VERSION AR350293.1 GI:33751264
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F., Baker,B.F., Wyatt,J. and Davis,S.E.
TITLE Antisense modulation of CD40 ligand expression
JOURNAL Patent: US 6586245-A 70 01-JUL-2003;
FEATURES
    source
        location/Qualifiers
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                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 9.13e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0
US-09-966-880A-8 (1-198) x AR350293 (1-20)
QY 2 AspSerLeuLeuMet 6
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Db 15 GACAGTCTTCTCATG 1

Search completed: March 5, 2004, 01:37:31
Job time : 3749 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 5, 2004, 01:37:34 ; Search time 351 Seconds
(without alignments)

2063.167 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198

Sequence: 1 MDSLLMRRKFLYQFNVRW.....ILLPLYEVDLDRFRTGL 198

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Searched: 2421054 seqs, 1828716029 residues

Word size: 1

Total number of hits satisfying chosen parameters: 446914

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

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c	2	6	3.0	19	15	US-10-349-143-7618	Sequence 7618, Ap
	3	6	3.0	20	15	US-10-349-143-9310	Sequence 9310, Ap
	4	6	3.0	21	15	US-10-289-762-5376	Sequence 5376, Ap
	5	5	2.5	15	10	US-09-877-478-6121	Sequence 6121, Ap
c	7	5	2.5	15	15	US-10-317-444-325	Sequence 325, App
	8	5	2.5	15	15	US-10-317-444-326	Sequence 326, App
c	9	5	2.5	15	15	US-10-317-444-479	Sequence 479, App
c	10	5	2.5	15	15	US-10-317-444-480	Sequence 480, App
c	11	5	2.5	16	9	US-09-873-075A-4	Sequence 4, Appli
	12	5	2.5	16	9	US-09-781-988-101	Sequence 101, App
c	13	5	2.5	16	10	US-09-771-933-189	Sequence 189, App
	14	5	2.5	16	10	US-09-893-878-101	Sequence 101, App
	15	5	2.5	16	11	US-09-896-095-101	Sequence 101, App
	16	5	2.5	16	15	US-10-126-685-101	Sequence 101, App
	17	5	2.5	16	15	US-10-127-028-101	Sequence 101, App
	18	5	2.5	16	16	US-10-126-544-101	Sequence 101, App
c	19	5	2.5	17	9	US-09-866-108-9581	Sequence 9581, Ap
c	20	5	2.5	17	9	US-09-866-108-9582	Sequence 9582, Ap
c	21	5	2.5	17	9	US-09-866-108-9583	Sequence 9583, Ap
	22	5	2.5	17	9	US-09-866-108-9630	Sequence 9630, Ap
	23	5	2.5	17	9	US-09-866-108-9631	Sequence 9631, Ap
	24	5	2.5	17	9	US-09-866-108-9632	Sequence 9632, Ap
	25	5	2.5	17	9	US-09-866-108-9765	Sequence 9765, Ap
	26	5	2.5	17	9	US-09-866-108-9766	Sequence 9766, Ap
	27	5	2.5	17	9	US-09-866-108-9767	Sequence 9767, Ap
c	28	5	2.5	17	10	US-09-825-803-345	Sequence 345, App
	29	5	2.5	17	10	US-09-730-289B-634	Sequence 634, App
c	30	5	2.5	17	10	US-09-818-875-1415	Sequence 1415, Ap
c	31	5	2.5	17	10	US-09-818-875-1416	Sequence 1416, Ap
	32	5	2.5	17	10	US-09-818-875-3818	Sequence 3818, Ap
c	33	5	2.5	17	10	US-09-818-875-3819	Sequence 3819, Ap
	34	5	2.5	17	10	US-09-780-533A-382	Sequence 382, App
c	35	5	2.5	17	10	US-09-780-533A-1219	Sequence 1219, Ap
c	36	5	2.5	17	10	US-09-780-533A-1263	Sequence 1263, Ap
c	37	5	2.5	17	10	US-09-780-533A-1373	Sequence 1373, Ap
c	38	5	2.5	17	10	US-09-780-533A-1374	Sequence 1374, Ap
c	39	5	2.5	17	10	US-09-780-533A-2240	Sequence 2240, Ap
	40	5	2.5	17	10	US-09-780-533A-2555	Sequence 2555, Ap
	41	5	2.5	17	10	US-09-877-478-280	Sequence 280, App
	42	5	2.5	17	10	US-09-877-478-373	Sequence 373, App
	43	5	2.5	17	10	US-09-877-478-374	Sequence 374, App
	44	5	2.5	17	10	US-09-877-478-1106	Sequence 1106, Ap
c	45	5	2.5	17	10	US-09-877-478-1486	Sequence 1486, Ap
				17	10	US-09-848-754A-967	Sequence 967, App

ALIGNMENTS

RESULT 1
US-10-349-143-11764
; Sequence 11764, Application US/10349143
; Publication No. US2004005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA


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; Sequence 6121, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6121
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6121

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-6121 (1-15)

QY 172 LeuSerArgGlnJeu 176
Db 1 CUUUCUGGCAACUU 15

RESULT 6
US-10-317-444-325
; Sequence 325, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12
US-10-317-444-325

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-325 (1-15)

QY 72 ProGlyArgCysTyr 76
Db 15 CCTGGACGGTGCTAC 1

RESULT 7
US-10-317-444-326/c
; Sequence 326, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12
US-10-317-444-326

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-326 (1-15)

QY 72 ProGlyArgCysTyr 76
Db 15 CCTGGACGGTGCTAC 1

RESULT 8
US-10-317-444-479
; Sequence 479, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7
US-10-317-444-479

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-479 (1-15)

QY 72 ProGlyArgCysTyr 76
|||||
DB 1 CCTGGACGGTGCTAC 15

RESULT 9
US-10-317-444-480/C
; Sequence 480, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 480
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7
US-10-317-444-480

Alignment Scores:
Pred. No.: 3.29e+03 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-317-444-480 (1-15)

QY 72 ProGlyArgCysTyr 76
|||||
DB 15 CCTGGACGGTGCTAC 1

RESULT 10
US-09-873-075A-4/C
; Sequence 4, Application US/09873075A
; Patent No. US20020123123A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873,075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-873-075A-4

Alignment Scores:
Pred. No.: 3.49e+03 Length: 16
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-873-075A-4 (1-16)

QY 70 LeuAspProGlyArg 74
|||||
DB 16 CTGGATCCAGGGCGT 2

RESULT 11
US-09-781-988-101
; Sequence 101, Application US/09781988
; Patent No. US20020150881A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20020150881A1el
Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
Suite 300
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/781,988
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,989
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-09-781-988-101

Alignment Scores:
Pred. No.: 3.49e+03 Length: 16
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-781-988-101 (1-16)

```
QY      178 ArgileLeuPro 182
Db      1 CGGATCCTCTCCT 15

RESULT 12
US-09-771-933-189/c
; Sequence 189, Application US/09771933
; Publication No. US20030023387A1
; GENERAL INFORMATION:
; APPLICANT: Gill-Garrison, Rosalynn D
; APPLICANT: Martin, Christopher J
; APPLICANT: Sanchez-Felix, Manuel V
; TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk
; FILE OF INVENTION: Factors
; FILE REFERENCE: 620-130
; CURRENT APPLICATION NUMBER: US/09/771,933
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 189
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-771-933-189

Alignment Scores:
Pred. No.:      3.49e+03      Length:      16
Score:          5.00          Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%       Indels:          0
DB:              10          Gaps:           0

US-09-966-880A-8 (1-198) x US-09-771-933-189 (1-16)

QY      25 ArgGluThrTyrLeu 29
Db      16 AGGAGACGATTG 2

RESULT 13
US-09-893-878-101
; Sequence 101, Application US/09893878
; Publication No. US20030113717A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsey
; Markland, William
; Lev, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20030113717A1e1
; Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,878
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; OTHER INFORMATION: synthetic, DNA for ID 10, lower strand, see also ID 16
US-09-896-880A-8 (1-198) x US-09-893-878-101 (1-16)

QY      178 ArgileLeuPro 182
Db      1 CGGATCCTCTCCT 15

RESULT 14
US-09-896-095-101
; Sequence 101, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEV, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic, DNA for ID 10, lower strand, see also ID 16
US-09-896-095-101
```

Alignment Scores: 3.49e-03 Length: 16
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 11

US-09-966-880A-8 (1-198) x US-09-896-095-101 (1-16)

Qy 178 ArgileLeuLeuPro 182
Db 1 CGGATCCTCTCCCT 15

RESULT 15

US-10-126-685-101
; Sequence 101, Application US/10126685
; Publication No. US20030219722A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsey
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20030219722A1e1
; Binding Proteins

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
Suite 300

CITY: Washington,

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/126,685

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/009,319

FILING DATE: 1993-01-26

APPLICATION NUMBER: 07/664,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 07/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28005

REFERENCE/DOCKET NUMBER: LADNER 7

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-126-685-101

Alignment Scores: 3.49e-03 Length: 16
Pred. No.: 5.00 Matches: 5
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Gaps: 0
DB: 15

US-09-966-880A-8 (1-198) x US-10-126-685-101 (1-16)

Qy 178 ArgileLeuLeuPro 182
Db 1 CGGATCCTCTCCCT 15

RESULT 16

US-10-127-028-101
; Sequence 101, Application US/10127028
; Publication No. US20040005539A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsey
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20040005539A1e1
; Binding Proteins

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
Suite 300

CITY: Washington,

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,028

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/009,319

FILING DATE: 1993-01-26

APPLICATION NUMBER: 07/664,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 01-SEP-1989

APPLICATION NUMBER: 07/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28005

REFERENCE/DOCKET NUMBER: LADNER 7

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-127-028-101

Alignment Scores:
Pred. No.: 3.49e+03 16
Score: 5.00 5
Matches: 0
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 2.53% 0
DB: 15 0

US-09-966-880A-8 (1-198) x US-10-127-028-101 (1-16)

QY 178 ArgileleuLeuPro 182
Db 1 CGGATCCTCTCCCT 15

RESULT 17

US-10-126-544-101
; Sequence 101, Application US/10126544
; Publication No. US20040023205A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsey
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20040023205A1el
; Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/126,544
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,319
; FILING DATE: 1993-01-26
; APPLICATION NUMBER: 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-10-126-544-101

Alignment Scores:
Pred. No.: 3.49e+03 16
Score: 5.00 5
Matches: 0
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 2.53% 0
DB: 16 0

US-09-966-880A-8 (1-198) x US-10-126-544-101 (1-16)

QY 178 ArgileleuLeuPro 182
Db 1 CGGATCCTCTCCCT 15

RESULT 18

US-09-866-108-9581/c
; Sequence 9581, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 9581
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9581

Alignment Scores:
Pred. No.: 3.69e+03 17
Score: 5.00 5
Matches: 0
Percent Similarity: 100.00%

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9581 (1-17)

QY 41 SerPheSerLeuAsp 45
DB 17 AGCTTTTCCCTCGAC 3

RESULT 19

US-09-866-108-9582/c
; Sequence 9582, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 9582
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9582

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9582 (1-17)

QY 41 SerPheSerLeuAsp 45
DB 16 AGCTTTTCCCTCGAC 2

RESULT 20

US-09-866-108-9583/c
; Sequence 9583, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 9583
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9583

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9583 (1-17)

QY 41 SerPheSerLeuAsp 45
DB 15 AGCTTTTCCCTCGAC 1

RESULT 21

US-09-966-108-9630
; Sequence 9630, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9630
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-966-108-9630

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9630 (1-17)

Oy 124 GluGlyLeuArgArg 128
Db 3 GAAGGGCTCCGGAGG 17

RESULT 22

US-09-866-108-9631
; Sequence 9631, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9631
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9631

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9631 (1-17)

Oy 124 GluGlyLeuArgArg 128
Db 2 GAAGGGCTCCGGAGG 16

RESULT 23

US-09-866-108-9632
; Sequence 9632, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

```

; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9632
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-9632

Alignment Scores:
Pred. No.: 3 69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9632 (1-17)

Qy 124 GluGlyLeuArg 128
| | | | | | | | | | | | | | | | | | | | |
Db 1 GAAGGGCTCGGAGG 15

RESULT 24
US-09-866-108-9765
; Sequence 9765, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108

```

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; FILE REFERENCE: AEOMICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9765
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-9765

Alignment Scores:
Pred. No.: 3 69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9765 (1-17)

Qy 103 AsnLeuSerLeuArg 107
| | | | | | | | | | | | | | | | | | | | |
Db 3 AACCTCTCGTGAGG 17

RESULT 25
US-09-866-108-9766
; Sequence 9766, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108

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;
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00660
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 9766
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9766

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9766 (1-17)

QY 103 AsnLeuSerLeuArg 107
|||||
Db 2 AACCTCTCGCTGAGG 16

RESULT 26
US-09-866-108-9767
; Sequence 9767, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

;
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 9767
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-9767

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108-9767 (1-17)

QY 103 AsnLeuSerLeuArg 107
|||||
Db 1 AACCTCTCGCTGAGG 15

RESULT 27
US-09-825-805-345
; Sequence 345, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucle
; FILE REFERENCE: MEH00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05

; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 345
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-345

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-825-805-345 (1-17)

Qy 89 AspCysAlaargHis 93
Db 3 GAUUGUGCGAGGCAC 17

RESULT 28

US-09-730-289B-634/c
; Sequence 634, Application US/09730289B
; Publication No. US20030050259A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
; FILE REFERENCE: MBH00-864-A (400/006)
; CURRENT APPLICATION NUMBER: US/09/730,289B
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/169,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 3897
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 634
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-730-289B-634

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-730-289B-634 (1-17)

Qy 165 LeuHisGluAsnSer 169
Db 16 CTACATGAGAAATCT 2

RESULT 29

US-09-818-875-1415
; Sequence 1415, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27

; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1415
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1415

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-1415 (1-17)

Qy 129 LeuHisArgAlaGly 133
Db 2 CTGCACCGGCGCGG 16

RESULT 30

US-09-818-875-1416/c
; Sequence 1416, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1416
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-1416

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-1416 (1-17)

Qy 129 LeuHisArgAlaGly 133
Db 16 CTGCACCGGCGCGG 2

RESULT 31

US-09-818-875-3818/c

; Sequence 3818, Application US/09818875
 ; Publication No. US20030051270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; APPLICANT: Rice, Michael C.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; TITLE OF INVENTION: Stranded Oligonucleotides
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/09/818,875
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 3818
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-818-875-3818

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-3818 (1-17)

Qy 93 HisValAlaAspPhe 97
 |||||
 Db 15 CATGTTGCAGACTTT 1

RESULT 32

US-09-818-875-3819
 ; Sequence 3819, Application US/09818875
 ; Publication No. US20030051270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; APPLICANT: Rice, Michael C.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; TITLE OF INVENTION: Stranded Oligonucleotides
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/09/818,875
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 3819
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-818-875-3819

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-818-875-3819 (1-17)

Qy 93 HisValAlaAspPhe 97
 |||||
 Db 3 CATGTTGCAGACTTT 17

RESULT 33

US-09-780-533A-382/c
 ; Sequence 382, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haeblerli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00.878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 382
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-382

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-382 (1-17)

Qy 169 SerValArgLeuSer 173
 |||||
 Db 16 TCAGTGAGACTTTCT 2

RESULT 34

US-09-780-533A-1219/c
 ; Sequence 1219, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haeblerli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH00.878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1219
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-1219

```

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1219 (1-17)

QY 58 GlulLeuLeuPheLeu 62
DB 16 GAGCTTCTGTTTCTT 2

RESULT 35
US-09-780-533A-1263/c
; Sequence 1263, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1263
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1263

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1263 (1-17)

QY 169 SerValArgLeuSer 173
DB 15 TCAGTGAGACTTCTT 1

RESULT 36
US-09-780-533A-1373/c
; Sequence 1373, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1373
; LENGTH: 17
; TYPE: RNA

```

```

; ORGANISM: Homo sapiens
US-09-780-533A-1373

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1373 (1-17)

QY 194 ArgThrLeuGlyLeu 198
DB 17 AGAACTTGGGTTTA 3

RESULT 37
US-09-780-533A-1374/c
; Sequence 1374, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1374
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1374

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-1374 (1-17)

QY 194 ArgThrLeuGlyLeu 198
DB 16 AGAACTTGGGTTTA 2

RESULT 38
US-09-780-533A-2240
; Sequence 2240, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0

```



```
; SEQ ID NO 2240
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2240

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-2240 (1-17)
QY 8 ArgArgLysPheLeu 12
Db 1 ACGAGAAAUCCUU 15

RESULT 39
US-09-780-533A-2555/c
; Sequence 2555, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrixa, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00-878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2555
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2555

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-780-533A-2555 (1-17)
QY 58 GluLeuLeuPheLeu 62
Db 15 GAGCTTCGTTCTT 1

RESULT 40
US-09-877-478-280
; Sequence 280, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
```

```
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-280

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-280 (1-17)
QY 172 LeuSerArgGlnLeu 176
Db 3 CUUUCUGGCACUU 17

RESULT 41
US-09-877-478-373
; Sequence 373, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 373
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
```

US-09-877-478-373

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-373 (1-17)

Qy 194 ArgThrLeuGlyLeu 198

 Db 3 AGGACUCUUGGACUU 17
 |||||

RESULT 42

US-09-877-478-374
 ; Sequence 374, Application US/09877478
 ; Publication No. US20030068301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Morrissey, Dave
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 ; FILE REFERENCE: MEHB00-845-H (400/029)
 ; CURRENT APPLICATION NUMBER: US/09/877,478
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: US 09/531,025
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: US 09/636,385
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 08/193,627
 ; PRIOR FILING DATE: 1994-02-07
 ; PRIOR APPLICATION NUMBER: US 08/433,993
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 08/434,504
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6586
 ; SEQ ID NO 374
 ; SOFTWARE: PatentIn version 3.0
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B virus
 US-09-877-478-374

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-374 (1-17)

Qy 194 ArgThrLeuGlyLeu 198

 Db 1 AGGACUCUUGGACUU 15
 |||||

RESULT 43

US-09-877-478-1106
 ; Sequence 1106, Application US/09877478
 ; Publication No. US20030068301A1
 ; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Morrissey, Dave
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 ; FILE REFERENCE: MEHB00-845-H (400/029)
 ; CURRENT APPLICATION NUMBER: US/09/877,478
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 09/531,025
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: US 09/636,385
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: US 09/696,347
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 08/193,627
 ; PRIOR FILING DATE: 1994-02-07
 ; PRIOR APPLICATION NUMBER: US 08/433,993
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 08/434,504
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1106
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Hepatitis B virus
 US-09-877-478-1106

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-877-478-1106 (1-17)

Qy 194 ArgThrLeuGlyLeu 198
 |||||

Db 2 AGGACUCUUGGACUU 16
 |||||

RESULT 44

US-09-877-478-1486
 ; Sequence 1486, Application US/09877478
 ; Publication No. US20030068301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Morrissey, Dave
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 ; FILE REFERENCE: MEHB00-845-H (400/029)
 ; CURRENT APPLICATION NUMBER: US/09/877,478
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 09/531,025
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: US 09/636,385
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: US 09/696,347
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 08/193,627
 ; PRIOR FILING DATE: 1994-02-07
 ; PRIOR APPLICATION NUMBER: US 08/433,993
 ; PRIOR FILING DATE: 1995-05-04

; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1486
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1486

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-877-478-1486 (1-17)

QY 172 LeuSerArgGlnLeu 176
|||||
Db 2 CUUUCUGCAACU 16

RESULT 45

US-09-848-754A-967/c
; Sequence 967, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 967
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-967

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-967 (1-17)

QY 129 LeuHisArgAlaGly 133
|||||
Db 17 TTGCACAGGCAGGG 3

RESULT 46

US-09-848-754A-968/c
; Sequence 968, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 968

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-968

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-968 (1-17)

QY 129 LeuHisArgAlaGly 133
|||||
Db 16 TTGCACAGGCAGGG 2

RESULT 47

US-09-848-754A-969/c
; Sequence 969, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 969
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-969

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-969 (1-17)

QY 129 LeuHisArgAlaGly 133
|||||
Db 15 TTGCACAGGCAGGG 1

RESULT 48

US-09-848-754A-2430/c
; Sequence 2430, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2430
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2430

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-848-754A-2430 (1-17)

QY 127 ArgArgLeuHisArg 131
DB 15 CGTAGGCTTCATCGA 1

RESULT 49

US-09-864-636A-789

; Sequence 789, Application US/09864636A

; Publication No. US20030104378A1

; GENERAL INFORMATION:

; APPLICANT: Third Wave Technologies

; APPLICANT: Allwail, Hatim

; APPLICANT: Bartholomay, Christian

; APPLICANT: Chehak, LuAnne

; TITLE OF INVENTION: Detection of RNA Sequences

; FILE REFERENCE: FORS-04944

; CURRENT APPLICATION NUMBER: US/09/864,636A

; CURRENT FILING DATE: 2002-10-15

; NUMBER OF SEQ ID NOS: 2640

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 789

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-09-864-636A-789

Alignment Scores:

Alignment Scores: Length: 17
Pred. No.: 3.69e+03 Matches: 5
Score: 5.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-636A-789 (1-17)

QY 70 LeuAspProGlyArg 74
DB 2 CTTGACCCAGGAGG 16

RESULT 50

US-09-864-636A-794

; Sequence 794, Application US/09864636A

; Publication No. US20030104378A1

; GENERAL INFORMATION:

; APPLICANT: Third Wave Technologies

; APPLICANT: Allwail, Hatim

; APPLICANT: Bartholomay, Christian

; APPLICANT: Chehak, LuAnne

; TITLE OF INVENTION: Detection of RNA Sequences

; FILE REFERENCE: FORS-04944

; CURRENT APPLICATION NUMBER: US/09/864,636A

; CURRENT FILING DATE: 2002-10-15

; NUMBER OF SEQ ID NOS: 2640

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 794

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-09-864-636A-794

Alignment Scores:

Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-636A-794 (1-17)

QY 70 LeuAspProGlyArg 74
DB 2 CTTGACCCAGGAGG 16

RESULT 51

US-09-740-332-1533

; Sequence 1533, Application US/09740332

; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel

; FILE REFERENCE: RPI 400/003

; CURRENT APPLICATION NUMBER: US/09/740,332

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9704

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1533

; LENGTH: 17

; TYPE: RNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-1533

Alignment Scores:

Alignment Scores: Length: 17
Pred. No.: 3.69e+03 Matches: 5
Score: 5.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-740-332-1533 (1-17)

QY 126 LeuArgArgLeuHis 130
DB 1 CUGAGGAGGUCCAU 15

RESULT 52

US-09-817-879-1533

; Sequence 1533, Application US/09817879

; Publication No. US20030171311A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel

; FILE REFERENCE: MBHE00-801-F

; CURRENT APPLICATION NUMBER: US/09/817,879

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9703

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1533

; LENGTH: 17

; TYPE: RNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION:

; OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-1533

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-817-879-1533 (1-17)

QY 126 LeuArgProGlyArg 130
|||||
Db 1 CUGAGGAGGCUCCAU 15

RESULT 53
US-09-864-426A-789
; Sequence 789, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichev, Victor
; APPLICANT: Saiser, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 789
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-789

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-426A-789 (1-17)

QY 70 LeuArgProGlyArg 74
|||||
Db 2 CTTGACCCAGGAGG 16

RESULT 54
US-09-864-426A-794
; Sequence 794, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichev, Victor
; APPLICANT: Saiser, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 794
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-794

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-864-426A-794 (1-17)

QY 70 LeuArgProGlyArg 74
|||||
Db 2 CTTGACCCAGGAGG 16

RESULT 55
US-10-297-134B-40/c
; Sequence 40, Application US/10297134B
; Publication No. US20040038233A1
; GENERAL INFORMATION:
; APPLICANT: Biomedlab
; TITLE OF INVENTION: diagnosis kit for Mycobacterium species identification and
; FILE REFERENCE: drug-resistance detection and manufacturing method thereof
; FILE REFERENCE: SG1601PCT
; CURRENT APPLICATION NUMBER: US/10/297,134B
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: KR10-2000-0029369
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 40
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Mycobacterium fortuitum, M. flavescens
US-10-297-134B-40

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-297-134B-40 (1-17)

QY 174 ArgGlnLeuArgArg 178
|||||
Db 17 CGACAGCTGCGACGT 3

RESULT 56
US-10-060-756A-1206
; Sequence 1206, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1206
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1206

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1206 (1-17)

Qy 172 LeuSerArgGlnLeu 176
 |||||
 Db 3 CTTTCCAGACAACTG 17

RESULT 57

US-10-060-756A-1207
 ; Sequence 1207, Application US/10060756A
 ; Publication No. US20030046717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Jian
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
 ; FILE REFERENCE: PB0177
 ; CURRENT APPLICATION NUMBER: US/10/060,756A
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1207
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1207

Alignment Scores:

Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1207 (1-17)

Qy 172 LeuSerArgGlnLeu 176
 |||||
 Db 2 CTTTCCAGACAACTG 16

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1207 (1-17)

Qy 172 LeuSerArgGlnLeu 176
 |||||
 Db 2 CTTTCCAGACAACTG 16

RESULT 58

US-10-060-756A-1208
 ; Sequence 1208, Application US/10060756A
 ; Publication No. US20030046717A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Jian
 ; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
 ; FILE REFERENCE: PB0177
 ; CURRENT APPLICATION NUMBER: US/10/060,756A
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/327,898
 ; PRIOR FILING DATE: 2001-10-09
 ; NUMBER OF SEQ ID NOS: 4804
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; SEQ ID NO 1208
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-060-756A-1208

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-060-756A-1208 (1-17)

Qy 172 LeuSerArgGlnLeu 176
 |||||
 Db 1 CTTTCCAGACAACTG 15

RESULT 59

US-10-163-552-111
 ; Sequence 111, Application US/10163552
 ; Publication No. US20030105051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, Jim
 ; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to lev
 ; TITLE OF INVENTION: HER2
 ; FILE REFERENCE: MEB01-1653-A (400/014)
 ; CURRENT APPLICATION NUMBER: US/10/163,552
 ; CURRENT FILING DATE: 2002-06-06
 ; NUMBER OF SEQ ID NOS: 1997
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 111
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-163-552-111

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-163-552-111 (1-17)
QY 89 AspCysAlaArgHis 93
DB 3 GAUUGUGCGAGGCAC 17
RESULT 60
US-10-156-306-247
; Sequence 247, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-247
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-156-306-247 (1-17)
QY 3 SerLeuLeuMetAsn 7
DB 1 UCGUGUCUUAUGAAU 15
RESULT 61
US-10-156-306-1470
; Sequence 1470, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1470
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1470
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-156-306-1470 (1-17)

QY 3 SerLeuLeuMetAsn 7
DB 2 UCGUGUCUUAUGAAU 16
RESULT 62
US-10-156-306-5016/c
; Sequence 5016, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5016
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5016
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-156-306-5016 (1-17)
QY 70 LeuAspProGlyArg 74
DB 17 CTCGATCCTGCGCGA 3
RESULT 63
US-10-156-306-7033/c
; Sequence 7033, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7033
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7033
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-156-306-7033 (1-17)
QY 70 LeuAspProGlyArg 74
DB 16 CTCGATCCTGCGCGA 2
RESULT 64

US-10-156-306-7034/c
; Sequence 7034, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSwiggan, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7034
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7034

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-306-7034 (1-17)
Qy 70 LeuAspProGlyArg 74
Db 15 CTCGATCTGGCGCA 1

RESULT 65
US-10-257-213-14
; Sequence 14, Application US/10257213
; Publication No. US20030129733A1
; GENERAL INFORMATION:
; APPLICANT: DENNING, David Wemys
; APPLICANT: BROOKMAN, Jayne Louise
; APPLICANT: RICKERS, Andre
; APPLICANT: BIRCH, Mike
; TITLE OF INVENTION: MUTANT BANK
; FILE REFERENCE: 31229-183869
; CURRENT APPLICATION NUMBER: US/10/257,213
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: GB0008748.6 PCT/GB01/01626
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-257-213-14

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-257-213-14 (1-17)
Qy 176 LeuArgGileLeu 180
Db 3 TTGAGCGAATTC 17

RESULT 66
US-10-339-782-104
; Sequence 104, Application US/10339782

Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lyrx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-104

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-339-782-104 (1-17)
Qy 179 IleLeuLeuProLeu 183
Db 2 ATGCTTCTGCTCTG 16

RESULT 67
US-10-061-201-1460
; Sequence 1460, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN PDSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 1460
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1460

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1460 (1-17)

OY 21 AlaLysGlyArg 25
DB 3 GCAAAAGGGAAGG 17

RESULT 68

US-10-061-201-1461
; Sequence 1461, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 1461
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-061-201-1461

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1461 (1-17)

OY 21 AlaLysGlyArg 25
DB 2 GCAAAAGGGAAGG 16

RESULT 69

US-10-061-201-1462
; Sequence 1462, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 1462
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-061-201-1462

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-061-201-1462 (1-17)

OY 21 AlaLysGlyArg 25
DB 1 GCAAAAGGGAAGG 15

RESULT 70

US-10-084-839-789
; Sequence 789, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: IP, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lyamacheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839

; CURRENT FILING DATE: 2002-02-26
 ; NUMBER OF SEQ ID NOS: 4004
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 789
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-084-839-789

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-839-789 (1-17)

QY 70 LeuAspProGlyArg 74
 DB 2 CTTGACCCAGGAGG 16

RESULT 71

US-10-084-839-794
 ; Sequence 794, Application US/10084839
 ; Publication No. US20030186238A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Third Wave Technologies
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Argue, Brad T.
 ; APPLICANT: Bartholomay, Christian T.
 ; APPLICANT: Chehak, LuAnne
 ; APPLICANT: Curtis, Michelle L.
 ; APPLICANT: Eis, Peggy S.
 ; APPLICANT: Hall, Jeff G.
 ; APPLICANT: IP, Hon S.
 ; APPLICANT: Ji, Lin
 ; APPLICANT: Kaiser, Michael
 ; APPLICANT: Kwiatkowski, Jr., Robert W.
 ; APPLICANT: Lukowiak, Andrew A.
 ; APPLICANT: Lymaicheva, Victor
 ; APPLICANT: Ma, WuPo
 ; APPLICANT: Neri, Bruce P.
 ; APPLICANT: Olson, Sarah M.
 ; APPLICANT: Olson-Munoz, Marilyn C.
 ; APPLICANT: Schaefer, James J.
 ; APPLICANT: Skrzypczynski, Zbigniew
 ; APPLICANT: Takova, Tsetska Y.
 ; APPLICANT: Thompson, Lisa C.
 ; APPLICANT: Vedvik, Kevin L.

; TITLE OF INVENTION: RNA Detection Assays
 ; FILE REFERENCE: FORS-06666
 ; CURRENT APPLICATION NUMBER: US/10/084,839
 ; CURRENT FILING DATE: 2002-02-26
 ; NUMBER OF SEQ ID NOS: 4004
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 794
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-084-839-794

Alignment Scores:
 Pred. No.: 3.69e+03 Length: 17
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-839-794 (1-17)

QY 70 LeuAspProGlyArg 74
 DB 2 CTTGACCCAGGAGG 16

RESULT 72

US-10-084-839-4004/c
 ; Sequence 4004, Application US/10084839
 ; Publication No. US20030186238A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Third Wave Technologies
 ; APPLICANT: Allawi, Hatim
 ; APPLICANT: Argue, Brad T.
 ; APPLICANT: Bartholomay, Christian T.
 ; APPLICANT: Chehak, LuAnne
 ; APPLICANT: Curtis, Michelle L.
 ; APPLICANT: Eis, Peggy S.
 ; APPLICANT: Hall, Jeff G.
 ; APPLICANT: IP, Hon S.
 ; APPLICANT: Ji, Lin
 ; APPLICANT: Kaiser, Michael
 ; APPLICANT: Kwiatkowski, Jr., Robert W.
 ; APPLICANT: Lukowiak, Andrew A.
 ; APPLICANT: Lymaicheva, Victor
 ; APPLICANT: Ma, WuPo
 ; APPLICANT: Neri, Bruce P.
 ; APPLICANT: Olson, Sarah M.
 ; APPLICANT: Olson-Munoz, Marilyn C.
 ; APPLICANT: Schaefer, James J.
 ; APPLICANT: Skrzypczynski, Zbigniew
 ; APPLICANT: Takova, Tsetska Y.
 ; APPLICANT: Thompson, Lisa C.
 ; APPLICANT: Vedvik, Kevin L.

; TITLE OF INVENTION: RNA Detection Assays
 ; FILE REFERENCE: FORS-06666
 ; CURRENT APPLICATION NUMBER: US/10/084,839
 ; CURRENT FILING DATE: 2002-02-26
 ; NUMBER OF SEQ ID NOS: 4004
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4004
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-084-839-4004

US-09-966-880A-8 (1-198) x US-10-084-839-4004 (1-17)

QY 178 ArgIleLeuLeuPro 182
 DB 17 CGAATTTTACTTCT 3

RESULT 73

US-10-209-787-1415
 ; Sequence 1415, Application US/10209787
 ; Publication No. US20030217377A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamber, Howard B.


```

; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3819
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-3819

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-209-787-3819 (1-17)

QY 93 HisValAlaAspPhe 97
Db 3 CATGTTCAGACTTT 17

RESULT 77
US-10-297-068-1106/c
; Sequence 1106, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1106
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1106

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-297-068-1106 (1-17)

QY 112 ArgLeuTyrPheCys 116
Db 15 CGCTTGCTACTTCTGT 1

RESULT 78
US-10-307-005-1007/c
; Sequence 1007, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:

```

```

; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1007
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-307-005-1007

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-307-005-1007 (1-17)

QY 32 valvalysargarg 36
Db 15 GTTGTCAAAAGGAGA 1

RESULT 79
US-10-307-005-1008
; Sequence 1008, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1008
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-307-005-1008

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17

```

5	
Matches:	5.00
Conservative:	100.00%
Mismatches:	100.00%
Indels:	2.53%
Gaps:	15
DB:	0
US-09-966-880A-B (1-198) x US-10-307-005-1008 (1-17)	

RESULT 83

```

US-10-261-185-1416/c
; Sequence 1416, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1416
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-261-185-1416

```

```

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

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US-09-966-880a-8 (1-198) x US-10-261-185-1416 (1-17)

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```

Qy 129 LeuHisArgAlaGly 133
|||||

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Db 16 CTGCACCGGCGCGG 2
|||||

```

RESULT 84

```

US-10-261-185-3818/c
; Sequence 3818, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3818
; LENGTH: 17

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-261-185-3818
Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

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US-09-966-880a-8 (1-198) x US-10-261-185-3818 (1-17)

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```

Qy 93 HisValAlaAspPhe 97
|||||

```

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Db 15 CATGTCGACACTTT 1
|||||

```

RESULT 85

```

US-10-261-185-3819
; Sequence 3819, Application US/10261185
; Publication No. US20040014057A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 3819
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-261-185-3819

```

```

Alignment Scores:
Pred. No.: 3.69e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

```

```

US-09-966-880a-8 (1-198) x US-10-261-185-3819 (1-17)

```

```

Qy 93 HisValAlaAspPhe 97
|||||

```

```

Db 3 CATGTCGACACTTT 17
|||||

```

RESULT 86

```

US-08-983-605-236/c
; Sequence 236, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400

```

/ CURRENT APPLICATION NUMBER: US/08/983,605A
/ CURRENT FILING DATE: 1998-05-01
/ EARLIER APPLICATION NUMBER: DE 195 25 284.5
/ EARLIER FILING DATE: 1995-06-28
/ NUMBER OF SEQ ID NOS: 466
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 236
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-08-983-605-236

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-983-605-236 (1-18)

Qy 70 LeuAspProGlyArg 74
Db 16 CTAGATCCCGGTGCA 2

RESULT 87
US-09-733-523-8
/ Sequence 8, Application US/09733523
/ Patent No. US20010044134A1
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE ZSIG87
/ FILE REFERENCE: 99-89
/ CURRENT APPLICATION NUMBER: US/09/733,523
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/169,597
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-733-523-8

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-733-523-8 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGCG 16

RESULT 88
US-09-122-383-3
/ Sequence 3, Application US/09122383A
/ Patent No. US20020042093A1
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Gilbertson, Debra G.
/ TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
/ FILE REFERENCE: 97-38
/ CURRENT APPLICATION NUMBER: US/09/122,383A

/ CURRENT FILING DATE: 1998-07-24
/ EARLIER APPLICATION NUMBER: 60/053,613
/ EARLIER FILING DATE: 1997-07-24
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide ZC976
US-09-122-383-3

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-122-383-3 (1-18)

Qy 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGCG 16

RESULT 89
US-09-923-246-77
/ Sequence 77, Application US/09923246
/ Patent No. US20020128446A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20020128446A1ak, Julia E.
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Gross, Jane A.
/ APPLICANT: Johnston, Janet V.
/ APPLICANT: Nelson, Andrew J.
/ APPLICANT: Dillon, Stacey R.
/ APPLICANT: Hammond, Angela K.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
/ FILE REFERENCE: 99-16
/ CURRENT APPLICATION NUMBER: US/09/923,246
/ CURRENT FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 77
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-923-246-77

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-923-246-77 (1-18)

Qy 32 ValVallysArgArg 36

```
Db      2 GTTGTAAACGACGG 16
RESULT 90
US-09-969-373-3238/c
; Sequence 3238, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3238
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3238
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3238 (1-18)

QY      101 AsnProAsnLeuSer 105
Db      18 AATCCAAATCTGAGT 4
RESULT 91
US-09-969-373-3240/c
; Sequence 3240, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3240
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3240
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3240 (1-18)

QY      101 AsnProAsnLeuSer 105
Db      18 AATCCAAATCTGAGT 4
RESULT 92
US-09-969-373-3489/c
; Sequence 3489, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3489
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3489
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0

US-09-966-880A-8 (1-198) x US-09-969-373-3489 (1-18)

QY      179 IleLeuLeuProLeu 183
Db      17 ATTCTGTGCCACTG 3
RESULT 93
US-09-969-373-3969
; Sequence 3969, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US 09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3969
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3969
Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             9          Gaps:        0
```


Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-969-373-3969 (1-18)
QY 93 HisValalaasphe 97
|||||
Db 1 CATGTAGCGACTTC 15
RESULT 94
US-09-969-373-4234
; Sequence 4234, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4234
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-4234
Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-969-373-4234 (1-18)
QY 101 AsnProAsnLeuSer 105
|||||
Db 4 AATCCCAATTGTCT 18
RESULT 95
US-09-978-600-172
; Sequence 172, Application US/09978600
; Publication No. US20030087858A1
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; PARKER, WILLIAM D.
; DAVIS, ROBERT
; MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; Animal Models for Diseases Associated With Mitochondrial
; Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 172:
US-09-978-600-172
Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-978-600-172 (1-18)
QY 125 GlyLeuArgArgLeu 129
|||||
Db 2 GGTCTACGAGGCTC 16
RESULT 96
US-09-746-375-44
; Sequence 44, Application US/09746375
; Publication No. US20030170823A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: NOVEL CYTOKINE ZCYTO18
; FILE REFERENCE: 99-106
; CURRENT APPLICATION NUMBER: US/09/746,375
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/172,105
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/****,***
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-746-375-44
Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-746-375-44 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 97

US-10-010-050A-3
; Sequence 3, Application US/10010050A
; Publication No. US20020173624A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul C.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
; TITLE OF INVENTION: CHROMOSOME 13
; FILE REFERENCE: 97-38C1
; CURRENT APPLICATION NUMBER: US/10/010,050A
; CURRENT FILING DATE: 2002-03-26
; PRIOR FILING DATE: 2002-03-26
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-10-010-050A-3

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-010-050A-3 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 98

US-10-086-135-7
; Sequence 7, Application US/10086135
; Publication No. US20020182677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: PANCREATIC AND OVARIAN POLYPEPTIDE
; TITLE OF INVENTION: ZSIG58
; FILE REFERENCE: 98-24
; CURRENT APPLICATION NUMBER: US/10/086,135
; CURRENT FILING DATE: 2002-02-26
; PRIOR FILING DATE: 2002-02-26
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-03
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-03
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer: ZC976
US-10-086-135-7

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-086-135-7 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 99

US-10-038-241-22
; Sequence 22, Application US/10038241
; Publication No. US20030032167A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; APPLICANT: Lofton-Day, Catherine E.
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: SECRETED ALPHA-HELICAL PROTEIN ZLMDA24
; FILE REFERENCE: 00-94
; CURRENT APPLICATION NUMBER: US/10/038,241
; CURRENT FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Sequence ZC976
US-10-038-241-22

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-038-241-22 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 100

US-10-197-290-10
; Sequence 10, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR FILING DATE: 2001-20-04
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
; LENGTH: 18

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-10

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-290-10 (1-18)
QY 59 LeuLeuPheLeuArg 63
Db 4 CTTTATTCTTAGA 18

RESULT 101
US-10-197-290-42
; Sequence 42, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2.
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/857,299
; PRIOR FILING DATE: 2001-20-04
; PRIOR APPLICATION NUMBER: PCT/US99/22083
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-42

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-290-42 (1-18)
QY 38 SerAlaThrSerPhe 42
Db 4 AGTGCTACCTCTTT 18

RESULT 102
US-10-127-816-20
; Sequence 20, Application US/10127816
; Publication No. US20030104416A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian A.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Taft, David W.
; APPLICANT: Kingsvoesi, Wayne R.
; TITLE OF INVENTION: CYTOKINE PROTEIN FAMILY
; FILE REFERENCE: 01-17
; CURRENT APPLICATION NUMBER: US/10/127,816

; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,408
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/286,482
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/341,050
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/341,105
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/285,424
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer 2C976
US-10-127-816-20

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-127-816-20 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 103
US-10-274-638-14
; Sequence 14, Application US/10274638
; Publication No. US20030109000A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIZED GROWTH FACTOR AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING IT
; FILE REFERENCE: 01-30
; CURRENT APPLICATION NUMBER: US/10/274,638
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/346,117
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer 2C976
US-10-274-638-14

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-274-638-14 (1-18)
QY 32 ValVallysArgArg 36

```

```
Db      2 GTTGTAAACGACGG 16

RESULT 104
US-10-295-723-77
; Sequence 77, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-295-723-77

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00         Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:       0
DB:             14           Gaps:         0

US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)
QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 105
US-10-282-622-24
; Sequence 24, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-282-622-24

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00         Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:       0
DB:             14           Gaps:         0

US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)
QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 106
US-10-313-739-32
; Sequence 32, Application US/10313739
; Publication No. US20030138948A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Fisk, Gregory
; APPLICANT: Inokuma, Margaret
; TITLE OF INVENTION: Islet Cells from Human Embryonic Stem Cells
; FILE REFERENCE: 132/002
; CURRENT APPLICATION NUMBER: US/10/313,739
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/338,885
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-313-739-32

Alignment Scores:
Pred. No.:      3.9e+03      Length:      18
Score:          5.00         Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    2.53%        Indels:       0
DB:             14           Gaps:         0

US-09-966-880A-8 (1-198) x US-10-313-739-32 (1-18)
QY      194 ArgThrLeuGlyLeu 198
Db      2 AGGACCTTGGGCTG 16

RESULT 107
US-10-243-072-6
; Sequence 6, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
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; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-243-072-6

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-243-072-6 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 108
US-10-321-164-19
; Sequence 19, Application US/10321164
; Publication No. US20030165530A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/10/321,164
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/552,225A
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-10-321-164-19

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-321-164-19 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 109
US-10-164-230-13
; Sequence 13, Application US/10164230
; Publication No. US20030170652A1
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
```

```
; APPLICANT: Tamiva, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112US1
; CURRENT APPLICATION NUMBER: US/10/164,230
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence
US-10-164-230-13

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-164-230-13 (1-18)
QY 128 ArgLeuHisArgala 132
Db 4 CGCCTCCACAGAGCT 18

RESULT 110
US-10-197-293-12
; Sequence 12, Application US/10197293
; Publication No. US20030171547A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49C1
; CURRENT APPLICATION NUMBER: US/10/197,293
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US 09/686,838
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/140,804
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/056,983
; PRIOR FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-10-197-293-12

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-197-293-12 (1-18)
QY 32 ValvallysargArg 36
Db 2 GTTGTAAACGACGG 16
```

```
RESULT 111
US-10-414-186-6
; Sequence 6, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-414-186-6

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-414-186-6 (1-18)

OY 32 ValVallyeArgArg 36
DB 2 GTTGTAACGACGG 16

RESULT 112
US-10-082-649-17
; Sequence 17, Application US/10082649
; Publication No. US20030176645A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/082,649
; FILING DATE: 22-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

US-09-966-880A-8 (1-198) x US-10-082-649-17 (1-18)

OY 129 LeuHisArgAlaGly 133
```

```
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC976
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-082-649-17

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-082-649-17 (1-18)

OY 32 ValVallyeArgArg 36
DB 2 GTTGTAACGACGG 16

RESULT 113
US-10-204-884-10
; Sequence 10, Application US/10204884
; Publication No. US20030186371A1
; GENERAL INFORMATION:
; APPLICANT: Oxagen Limited
; APPLICANT: Olaveson, Mark
; APPLICANT: Lench, Nick
; APPLICANT: Allen, Maxine
; APPLICANT: Tazi-Ahmini, Rachid
; TITLE OF INVENTION: Test and model for inflammatory disease
; FILE REFERENCE: P30000WO-PS
; CURRENT APPLICATION NUMBER: US/10/204,884
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: GB 0004312.5
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-204-884-10

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-204-884-10 (1-18)

OY 129 LeuHisArgAlaGly 133
```

Db 3 CTCACAGAGCTGGA 17
|||||
RESULT 114
US-10-204-884-77
; Sequence 77, Application US/10204894
; Publication No. US20030186371A1
; GENERAL INFORMATION:
; APPLICANT: Oxagen Limited
; APPLICANT: Olaveson, Mark
; APPLICANT: Lench, Nick
; APPLICANT: Allen, Maxine
; APPLICANT: Tazi-Ahmini, Rachid
; TITLE OF INVENTION: Test and model for inflammatory disease
; FILE REFERENCE: P300000-PS
; CURRENT APPLICATION NUMBER: US/10/204,884
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: GB 0004312.5
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-204-884-77
Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880a-8 (1-198) x US-10-204-884-77 (1-18)
QY 129 LeuHisArgAlaGly 133
|||||
Db 3 CTCACAGAGCTGGA 17
|||||
RESULT 115
US-10-388-263-163
; Sequence 163, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-163

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0
US-09-966-880a-8 (1-198) x US-10-388-263-163 (1-18)
QY 59 LeuLeuPheLeuArg 63
|||||
Db 4 CTTTATTCTTACA 18
|||||
RESULT 116
US-10-388-263-195
; Sequence 195, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-195
Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0
US-09-966-880a-8 (1-198) x US-10-388-263-195 (1-18)
QY 38 SerAlaThrSerPhe 42
|||||
Db 4 AGCTACCTCTTT 18
|||||
RESULT 117
US-10-388-263-244/c
; Sequence 244, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.

```

; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-244

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-263-244 (1-18)

Qy 103 AsnLeuSerIeuArg 107
Db 17 AACCTTCTCTCAGA 3

RESULT 118
US-10-349-143-6619
; Sequence 6619, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6619
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in compl
US-10-349-143-6619

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-6619 (1-18)

Qy 103 AsnLeuSerIeuArg 107
Db 17 AACCTTCTCTCAGA 3

RESULT 118
US-10-349-143-6619
; Sequence 6619, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6619
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-14074 for SEQ 2685,
US-10-349-143-6619

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-6619 (1-18)

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Qy 102 ProAsnLeuSerIeu 106
Db 4 CCAAATCTATCCCTC 18

RESULT 119
US-10-349-143-10343
; Sequence 10343, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in compl
US-10-349-143-10343

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-349-143-10343 (1-18)

Qy 34 LysArgArgAspSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 120
US-10-395-741B-44
; Sequence 44, Application US/10395741B
; Publication No. US20040023341A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Hughes, Steven D.
; APPLICANT: Chandrasekhar, Yasmin A.
; TITLE OF INVENTION: ANTI-IL-1/TIF ANTIBODIES AND METHODS OF
; FILE REFERENCE: 02-04
; CURRENT APPLICATION NUMBER: US/10/395,741B
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/366,842
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer 2C976

```


US-10-395-741B-44

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-395-741B-44 (1-18)

QY 32 ValVallyeArgArg 36

Db 2 GTTGTAACGACGG 16

RESULT 121

US-10-621-787-19
Sequence 19, Application US/10621787
Publication No. US20040024187A1
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
FILE REFERENCE: ZACRP2
CURRENT APPLICATION NUMBER: US/10/621,787
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 09/552,204
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: US 60/130,207
PRIOR FILING DATE: 1993-04-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC976
US-10-621-787-19

Alignment Scores:
Pred. No.: 3.9e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-621-787-19 (1-18)

QY 32 ValVallyeArgArg 36

Db 2 GTTGTAACGACGG 16

RESULT 122

US-09-912-014-21
Sequence 21, Application US/09912014
Publication No. US2003005929A1
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC SYSTEMS AND DEVICES FOR DIAGNOSTICS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,014
FILING DATE: 24-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146,504
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-912-014-21

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-912-014-21 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGAACTGCTC 16

RESULT 123

US-10-388-703-16
Sequence 16, Application US/10388703
Publication No. US20040029145A1
GENERAL INFORMATION:
APPLICANT: Rothschild, Max
APPLICANT: Kim, Kwan-Suk
APPLICANT: Neuyet-Thu, Nguyen
TITLE OF INVENTION: No. US20040029145A1 HMG A Alleles and Use of Same as Genetic M.
FILE REFERENCE: ISURF 2900
CURRENT APPLICATION NUMBER: US/10/388,703
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/364,959
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 19
TYPE: DNA
ORGANISM: porcine
US-10-388-703-16

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-703-16 (1-19)

QY 37 AspSerAlaThrSer 41
|||||

Db 2 GACTCAGCAACCTCC 16

RESULT 124

US-10-388-703-18

; Sequence 18, Application US/10388703

; Publication No. US20040029145A1

; GENERAL INFORMATION:

; APPLICANT: Rothschild, Max

; APPLICANT: Kim, Kwan-Suk

; APPLICANT: Neuvelet-Thu, Nguyen

; TITLE OF INVENTION: No. US20040029145A1el HMGA Alleles and Use of Same as Genetic Marker

; TITLE OF INVENTION: Quality, and Feed Efficiency Traits

; FILE REFERENCE: ISURF 2900

; CURRENT APPLICATION NUMBER: US/10/388,703

; PRIOR FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: 60/364,959

; PRIOR FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 19

; TYPE: DNA

; ORGANISM: porcine

US-10-388-703-18

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-388-703-18 (1-19)

QY 37 AspSerAlaThrSer 41
|||||

Db 2 GACTCAGCAACCTCC 16

RESULT 125

US-10-398-308-127/c

; Sequence 127, Application US/10398308

; Publication No. US20040029825A1

; GENERAL INFORMATION:

; APPLICANT: Davies, Christopher J.

; APPLICANT: Schlaifer, Donald H.

; APPLICANT: Hill, Jonathan R.

; TITLE OF INVENTION: METHODS OF MINIMIZING IMMUNOLOGICAL REJECTION OF A

; TITLE OF INVENTION: NUCLEAR TRANSFER FETUS

; FILE REFERENCE: 19603/3373

; CURRENT APPLICATION NUMBER: US/10/398,308

; CURRENT FILING DATE: 2003-04-03

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: PCT/US01/30925

; PRIOR FILING DATE: 2001-10-03

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 127

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: BOLA Class I,

; OTHER INFORMATION: Exon 3, Series B Probe

US-10-398-308-127

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-398-308-127 (1-19)

QY 104 LeuSerLeuArgIle 108
|||||

Db 17 CTGCTCTCCGATC 3

RESULT 126

US-10-146-575-44

; Sequence 44, Application US/10146575

; Publication No. US20030059800A1

; GENERAL INFORMATION:

; APPLICANT: Lichter, Jay

; APPLICANT: Guido, Marco

; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4

; FILE REFERENCE: SEQ-12P

; CURRENT APPLICATION NUMBER: US/10/146,575

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: US/09/144,367

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 44

; LENGTH: 19

; TYPE: DNA

; ORGANISM: H. sapiens

US-10-146-575-44

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-146-575-44 (1-19)

QY 22 LysGlyArgGlu 26
|||||

Db 3 AAGGCGAGGAGAG 17

RESULT 127

US-10-020-695-16/c

; Sequence 16, Application US/10020695

; Publication No. US20030140355A1

; GENERAL INFORMATION:

; APPLICANT: KIM, Dong-Soo

; APPLICANT: NAM, Yoon-Kwon

; APPLICANT: NOH, Jae-Koo

; TITLE OF INVENTION: EXPRESSION VECTOR CONTAINING LECTIN GENE REGULATION SITE OF MUD

; TITLE OF INVENTION: LOACH

; FILE REFERENCE: PPBA0566

; CURRENT APPLICATION NUMBER: US/10/020,695

; CURRENT FILING DATE: 2001-12-12

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Kapatentin 1.71

; SEQ ID NO 16

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer for detecting a lectin gene regulation site of a mud loa

US-10-020-695-16

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-020-695-16 (1-19)

QY 162 TtPgluGlyLeuHis 166

Db 18 TGAGGAGGACTGCAT 4

RESULT 128

US-10-371-066-21

; Sequence 21, Application US/10371066

; Publication No. US20030162214A1

; GENERAL INFORMATION:

; APPLICANT: Heller, Michael J.; and Tu, Eugene

; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING

; MICROELECTRONIC SYSTEMS AND DEVICES FOR

; MOLECULAR BIOLOGICAL ANALYSIS AND

; DIAGNOSTICS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM compatible

; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/371,066

; FILING DATE: 21-Feb-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/146,504

; FILING DATE: 08/08/146,504

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 203/218

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-371-066-21

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-371-066-21 (1-19)

QY 56 HisValGluLeuLeu 60

Db 2 CACGTAGACTGCTC 16

RESULT 129

US-10-221-917-1/c

; Sequence 1, Application US/10221917

; Publication No. US20030171570A1

; GENERAL INFORMATION:

; APPLICANT: Schweitzer, Markus

; TITLE OF INVENTION: Reactive Monomers For The Oligonucleotide and

; Polynucleotide Synthesis, Modified Oligonucleotides And

; Polynucleotides, and A Method For Producing The Same

; FILE REFERENCE: 200404.us

; CURRENT APPLICATION NUMBER: US/10/221,917

; PRIOR FILING DATE: 2003-01-13

; PRIOR APPLICATION NUMBER: PCT/EP01/01799

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polynucleotides

; OTHER INFORMATION: from modified acetals and aldehydes

US-10-221-917-1

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.53%

Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-221-917-1 (1-19)

QY 56 HisValGluLeuLeu 60

Db 18 CACGTAGACTGCTC 4

RESULT 130

US-10-170-172-21

; Sequence 21, Application US/10170172

; Publication No. US20030190632A1

; GENERAL INFORMATION:

; APPLICANT: SOSNOWSKI, RONALD G

; APPLICANT: BUTLER, WILLIAM F

; APPLICANT: TU, EUGENE

; APPLICANT: NERENBERG, MICHAEL I

; APPLICANT: HELLER, MICHAEL J

; APPLICANT: EDMAN, CARL P

; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC

; INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,

; METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL

; ANALYSIS AND DIAGNOSTICS

; FILE REFERENCE: DAVID B. MURPHY; Nanogen 227/194

; CURRENT APPLICATION NUMBER: US/10/170,172

; CURRENT FILING DATE: 2002-06-11

; PRIOR APPLICATION NUMBER: US/08/986,065

; PRIOR FILING DATE: 1997-12-05

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Human

US-10-170-172-21

Alignment Scores:

Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.53%

Indels: 0

DB: 14 Gaps: 0

Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-21 (1-19)

QY 56 HisValGlulLeuLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 131
US-10-170-172-45/c
; Sequence 45, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; TITLE OF INVENTION: ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; PRIOR FILING DATE: 2002-06-11
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human
US-10-170-172-45

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-45 (1-19)

QY 56 HisValGlulLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 132
US-10-170-172-50/c
; Sequence 50, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; TITLE OF INVENTION: ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 50
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human
US-10-170-172-50

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-50 (1-19)

QY 56 HisValGlulLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 133
US-10-170-221-20
; Sequence 20, Application US/10170221
; Publication No. US20030192068A1
; GENERAL INFORMATION:
; APPLICANT: DeBoer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/170,221
; FILING DATE: 11-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,798
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/077,788
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: US 07/895,956
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 07/619,131
; FILING DATE: 27-NOV-1990
; APPLICATION NUMBER: US 07/444,745
; FILING DATE: 01-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-170-221-20

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-221-20 (1-19)

Qy 32 ValVallyeArgArg 36
Db 5 GTTGTAAACGACGG 19

RESULT 134

US-10-244-647-467
Sequence 467, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SEQ ID NO 467
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

US-10-244-647-467

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-467 (1-19)

Qy 172 LeuSerArgGlnLeu 176
Db 2 CUUUCUGCCAACTU 16

RESULT 135

US-10-244-647-469
Sequence 469, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David

APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 469
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

US-10-244-647-469

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-469 (1-19)

Qy 172 LeuSerArgGlnLeu 176
Db 1 CUUUCUGCCAACTU 15

RESULT 136

US-10-244-647-1113/C
Sequence 1113, Application US/10244647
Publication No. US20030206887A1
GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MBHB02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1113
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-244-647-1113

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-1113 (1-19)

QY 172 LeuSerArgGlnLeu 176
DB 18 CTTTCGCGCAACTT 4

RESULT 137

US-10-244-647-1115/c
; Sequence 1115, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; TITLE OF INVENTION: Short Interfering Nucleic Acid (siRNA)
; FILE REFERENCE: 400/060 (MBH02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1115
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
US-10-244-647-1115

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-244-647-1115 (1-19)

QY 172 LeuSerArgGlnLeu 176
DB 19 CTTTCGCGCAACTT 5

RESULT 138

US-10-444-925-459
; Sequence 459, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Stephen Patrick
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Wilson, Linda K.
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
; TITLE OF INVENTION: BY RNA INTERFERENCE
; FILE REFERENCE: 200125.441
; CURRENT APPLICATION NUMBER: US/10/444,925
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 459
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-459

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-925-459 (1-19)

QY 119 ArgLysAlaGluPro 123
DB 4 AGGAAGCGAGAGCCC 18

RESULT 139

US-10-444-925-570
; Sequence 570, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Stephen Patrick
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Wilson, Linda K.
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
; TITLE OF INVENTION: BY RNA INTERFERENCE
; FILE REFERENCE: 200125.441
; CURRENT APPLICATION NUMBER: US/10/444,925
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-570

Alignment Scores:
Pred. No.: 4.1e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-925-570 (1-19)

QY 125 GlyLeuArgGlnLeu 129
DB 4 GGUCUGCGGCGUUA 18

RESULT 140

US-09-764-050A-2
; Sequence 2, Application US/09764050A
; Patent No. US2002068282A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Detection/Quantification of Targeted Nucleotide Chains and
; TITLE OF INVENTION: Detection/Quantification of Multi-Stranded Nucleotide Chains
; TITLE OF INVENTION: by Fluorescence
; FILE REFERENCE: 3495015
; CURRENT APPLICATION NUMBER: US/09/764,050A
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthesized
US-09-764-050A-2

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-764-050A-2 (1-20)

Qy 32 ValVallysArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 141
US-09-416-384A-12
; Sequence 12, Application US/09416384A
; Patent No. US20020081584A1
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BOUGUELBRET, Lydie
; APPLICANT: CHUMAKOV, Ilya
; APPLICANT: COHEN, Daniel
; APPLICANT: ESSIUX, Laurent
; TITLE OF INVENTION: Genes, proteins and biallelic markers related to central....
; FILE REFERENCE: GENSET.045AUS
; CURRENT FILING DATE: 1999-10-12
; CURRENT APPLICATION NUMBER: US/09/416,384A
; PRIOR FILING DATE: 1999-10-30
; PRIOR APPLICATION NUMBER: 60/106,457
; PRIOR FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: 60/103,955
; PRIOR FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: 60/132,277
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent.pm
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide g713RACE5R1
US-09-416-384A-12

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-416-384A-12 (1-20)

Qy 23 GlyArgArgGluThr 27
Db 2 GGTAGAAGGGAGACT 16

RESULT 142
US-09-731-457B-79/c
; Sequence 79, Application US/09731457B
; Patent No. US20020103146A1
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1,
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0182
; CURRENT APPLICATION NUMBER: US/09/731,457B
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-731-457B-79

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-731-457B-79 (1-20)

Qy 42 PheSerLeuAspPhe 46
Db 20 TTCTCCCTGGATTTT 6

RESULT 143
US-09-971-309-67
; Sequence 67, Application US/09971309
; Patent No. US20020106675A1
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko
; APPLICANT: MIYAKE, Kazue
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-0494P
; CURRENT APPLICATION NUMBER: US/09/971,309
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/446,504
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-971-309-67

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-971-309-67 (1-20)

Qy 156 GluArgThrPheLys 160

Db 3 GAGAGAACTTCAAG 17
|||||
RESULT 144
US-09-781-988-104/c
; Sequence 104, Application US/09781988
; Patent No. US20020150881A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Barbault
; TITLE OF INVENTION: Directed Evolution of No. US20020150881A1e1
; Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/781,988
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/664,989
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-781-988-104
Alignment Scores: 20
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-781-988-104 (1-20)
Qy 178 ArgilleLeuPro 182
Db 18 CGGATCCTCTCGCT 4
|||||
RESULT 145

US-09-900-063-6
; Sequence 6, Application US/09900063
; Patent No. US20020160372A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; Applicant: Vincent, Amy L.
; APPLICANT: Tuggle, Christopher K.
; TITLE OF INVENTION: Prolactin Receptor Gene as a Genetic Marker for
; TITLE OF INVENTION: Increased Litter Size in Pigs
; FILE REFERENCE: Prolactin receptor genetic marker
; CURRENT APPLICATION NUMBER: US/09/900,063
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/274,655
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/812,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/742,805
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/022180
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: porcine
US-09-900-063-6
Alignment Scores: 20
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-900-063-6 (1-20)
Qy 177 ArgArgilleLeuLeu 181
Db 5 CGCAGATCCTCGTG 19
|||||
RESULT 146
US-09-963-875-27/c
; Sequence 27, Application US/09963875
; Patent No. US20020164307A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treatin
; FILE REFERENCE: Mellitus
; FILE REFERENCE: 17633/1235
; CURRENT APPLICATION NUMBER: US/09/963,875
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US60/169082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/215109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/238880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731261
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-963-875-27
Alignment Scores: 20
Pred. No.: 4.3e+03 Length: 20

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-963-875-27 (1-20)

Qy 59 LeuLeupheLeuArg 63
Db 18 TTGCTGTTCTTCGG 4

RESULT 147

US-09-309-196-44/c
; Sequence 44, Application US/09309196
; Publication No. US2003008380A1
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,196
; FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/322,137

FILING DATE:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328

FILING DATE: 31-JAN-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431

FILING DATE: 31-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.

REGISTRATION/DOCKET NUMBER: 28,005

REFERENCE/DOCKET NUMBER: FOWLKES=2C

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-309-196-44

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-309-196-44 (1-20)

Qy 104 LeuSerLeuArgile 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 148

US-09-931-375A-52
; Sequence 52, Application US/09931375A
; Publication No. US20030027151A1
; GENERAL INFORMATION:
; APPLICANT: WARMAN, Matthew L.
; APPLICANT: GONG, Yaogin
; APPLICANT: OLSEN, Bjorn R.
; APPLICANT: RAWADI, Georges
; APPLICANT: ROMAN-ROMAN, Sergio
; TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 38464-0004
; CURRENT APPLICATION NUMBER: US/09/931,375A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/304,851
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/234,337
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/226,119
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer

US-09-931-375A-52

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-931-375A-52 (1-20)

Qy 168 AsnSerValArgLeu 172
Db 4 AACAGTCTCCGCTG 18

RESULT 149

US-09-972-115A-26
; Sequence 26, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-972-115A-26

Alignment Scores:
Pred. No.: 4.3e+03
Score: 5.00
Length: 20
Percent Similarity: 100.00%
Matches: 5
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0
Gaps: 0
DB: 10

US-09-966-880A-8 (1-198) x US-09-972-115A-26 (1-20)

QY 25 ArgGluThrLeu 29
Db 5 CGAGAGACTATCTC 19

RESULT 150
US-09-953-354-47/c
; Sequence 47, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; TITLE OF INVENTION: Methods and Compositions for
; Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,354
; FILING DATE: 13-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/689,172
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-953-354-47

Alignment Scores:
Pred. No.: 4.3e+03
Score: 5.00
Length: 20
Percent Similarity: 100.00%
Matches: 5
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0
Gaps: 0
DB: 10

US-09-966-880A-8 (1-198) x US-09-953-354-49 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 151
US-09-953-354-49/c
; Sequence 49, Application US/09953354
; Publication No. US20030054402A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; TITLE OF INVENTION: Methods and Compositions for
; Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,354
; FILING DATE: 13-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/689,172
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: CPI-012CP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-953-354-49

Alignment Scores:
Pred. No.: 4.3e+03
Score: 5.00
Length: 20
Percent Similarity: 100.00%
Matches: 5
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0
Gaps: 0
DB: 10

US-09-966-880A-8 (1-198) x US-09-953-354-49 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 152
US-09-912-014-7/c
; Sequence 7, Application US/09912014
```

```
; Publication No. US20030059929A1
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; MICROELECTRONIC SYSTEMS AND DEVICES FOR
; MOLECULAR BIOLOGICAL ANALYSIS AND
; DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/912,014
; FILING DATE: 24-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-912-014-7
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-912-014-7 (1-20)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGACTGCTC 4
RESULT 153
US-09-865-993-61
; Sequence 61, Application US/09865993
; Publication No. US20030060437A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5 EXPRESSION
; FILE REFERENCE: RTS-0175
; CURRENT APPLICATION NUMBER: US/09/865,993
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-993-61
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-865-993-61 (1-20)
Qy 39 AlaThrSerPheSer 43
Db 4 GCAACTTCTTTCTCC 18
RESULT 154
US-09-909-595-70/c
; Sequence 70, Application US/09909595
; Publication No. US20030083278A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-70
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-909-595-70 (1-20)
Qy 2 AspSerLeuLeuMet 6
Db 15 GACAGTCTTCTCATG 1
RESULT 155
US-09-915-485-58
; Sequence 58, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/915,485
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```
US-09-915-485-58
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-915-485-58 (1-20)
QY 42 PheSerLeuAspPhe 46
Db 3 TTCTCGTTGGACTTC 17

RESULT 156
US-09-918-187-28/c
; Sequence 28, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-28
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-918-187-28 (1-20)
QY 125 GlyLeuArgGlnLeu 129
Db 19 GGCTTGAGAGGTTA 5

RESULT 157
US-09-918-187-29/c
; Sequence 29, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-29
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5

us-09-966-880a-8.Oligo.rnpb
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-918-187-29 (1-20)
QY 172 LeuSerArgGlnLeu 176
Db 16 CTGTCCAGGCAGCTC 2

RESULT 158
US-09-915-814-178/c
; Sequence 178, Application US/09915814
; Publication No. US20030096771A1
; GENERAL INFORMATION:
; APPLICANT: Mageline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0587
; CURRENT APPLICATION NUMBER: US/09/915,814
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-814-178
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-915-814-178 (1-20)
QY 129 LeuHisArgAlaGly 133
Db 16 CTCATCGGCTGTGT 2

RESULT 159
US-09-893-878-104/c
; Sequence 104, Application US/09893878
; Publication No. US20030113717A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20030113717A1e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,878
FILING DATE: 29-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,319
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-893-878-104

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-893-878-104 (1-20)

QY 178 ArgileLeuPro 182
Db 18 CGATCTCTCTCCT 4

RESULT 160
US-09-851-871-69
Sequence 69, Application US/09851871
Publication No. US20030176374A1
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Karras, James G.
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
FILE REFERENCE: ISPH-0543
CURRENT APPLICATION NUMBER: US/09/851,871
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: PCT/US00/14471
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/777,266
PRIOR FILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 69
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic

OTHER INFORMATION: Synthetic
US-09-851-871-69
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-851-871-69 (1-20)

QY 176 LeuArgArgLeu 180
Db 1 CTGCGCGAATCCTG 15

RESULT 161
US-09-851-871-166
Sequence 166, Application US/09851871
Publication No. US20030176374A1
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
FILE REFERENCE: ISPH-0543
CURRENT APPLICATION NUMBER: US/09/851,871
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: PCT/US00/14471
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/326,186
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/777,266
PRIOR FILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 166
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-851-871-166 (1-20)

QY 176 LeuArgArgLeu 180
Db 2 CTGCGCGAATCCTG 16

RESULT 162
US-09-865-879-35/c
Sequence 35, Application US/09865879
Publication No. US20030180707A1
GENERAL INFORMATION:
APPLICANT: Roninson, Igor
APPLICANT: Dokmanovic, Milos
TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION
FILE REFERENCE: 99,216-H
CURRENT APPLICATION NUMBER: US/09/865,879
CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense primer for HIF-2alpha/ EPAS-1
US-09-865-879-35

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-865-879-35 (1-20)

QY 43 SerLeuAappheCly 47
| | | | | | | | | | | | | | | | | | | | | |
Db 15 TCTCTGGATTCTGGG 1

RESULT 163

US-09-896-095-104/c
; Sequence 104, Application US/09896095
; Publication No. US2003021986A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic, DNA for ID 10, M13.3X7
US-09-896-095-104

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-896-095-104 (1-20)

QY 178 ArgileLeuPro 182
| | | | | | | | | | | | | | | | | | | | | |
Db 18 CGGATCTCTCTCCT 4

RESULT 164

US-10-188-186-294/c
; Sequence 294, Application US/10188186
; Publication No. US20040029789A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-397C
; CURRENT APPLICATION NUMBER: US/10/188,186
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/360814
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/303828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/323380
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/361133
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: 60/304016
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/373881
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/305673
; PRIOR FILING DATE: 2001-07-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: Custom
; SEQ ID NO 294
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reverse Primer
US-10-188-186-294

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-186-294 (1-20)

Cy 94 ValAlaAappheLeu 98
| | | | | | | | | | | | | | | | | | | | | |
Db 18 GTTGCTGACTTCCTG 4

RESULT 165

US-10-005-964-4/c
; Sequence 4, Application US/10005964
; Publication No. US20020107219A1
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Yamamoto, Masato
; TITLE OF INVENTION: Adenoviral Vector Containing Cyclooxygenase-2
; TITLE OF INVENTION: Promoter And Uses Thereof
; FILE REFERENCE: D6384
; CURRENT APPLICATION NUMBER: US/10/005,964
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,375
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: primer_bind
; OTHER INFORMATION: GAPDH antisense primer
US-10-005-964-4

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-005-964-4 (1-20)
QY 82 ThrSerTpSerPro 86
DB 20 ACGTCGTGGAGTCGA 6

RESULT 166
US-10-136-891-25/c
; Sequence 25, Application US/10136891
; Publication No. US20030031657A1
; GENERAL INFORMATION:
; APPLICANT: Habener, Joel
; TITLE OF INVENTION: STEM CELLS AND THEIR USE IN TRANSPLANTATION
; FILE REFERENCE: 3284/1225
; CURRENT APPLICATION NUMBER: US/10/136,891
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/169,082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/215,109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/239,880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731,255
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-136-891-25

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-136-891-25 (1-20)
QY 59 LeuLeuPheLeuArg 63
DB 18 TTGCTGTTTCTTCGG 4

RESULT 167
US-10-057-550-93
; Sequence 93, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-93

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-057-550-93 (1-20)
QY 169 SerValArgLeuSer 173
DB 4 TCTGTAAAGCCTTCA 18

RESULT 168
US-10-084-406-11/c
; Sequence 11, Application US/10084406
; Publication No. US20030054525A1
; GENERAL INFORMATION:
; APPLICANT: Schwientek, Tilo
; TITLE OF INVENTION: UPD-N-Acetylglucosamine:
Galactose-beta1,3-N-Acetylgalactoseamine-alpha-R / (GlcNAc
; TITLE OF INVENTION: Galactose-beta1,3-N-Acetylgalactoseamine-alpha-R / (GlcNAc
; TITLE OF INVENTION: to GalNAc) beta1,6-N-Acetylglucosamineyltransferase, C2Gnt3
; FILE REFERENCE: 4503/1G031
; CURRENT APPLICATION NUMBER: US/10/084,406
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/645,192
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-084-406-11

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-084-406-11 (1-20)
QY 125 GlyLeuArgArgLeu 129
```

```
Db      18 GGGTTGAGGACTG 4
|||||
RESULT 169
US-10-120-687-27/c
; Sequence 27, Application US/10120687
; Publication No. US20030082155A1
; GENERAL INFORMATION:
; APPLICANT: Massachusetts General Hospital
; TITLE OF INVENTION: Stem Cells of the Islets of Langerhans and Their Use in Treating
; TITLE OF INVENTION: Mellitus
; FILE REFERENCE: 3284/1235B
; CURRENT APPLICATION NUMBER: US/10/120,687
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US60/169082
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/963,875
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/215109
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: US 60/238880
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/731261
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Synthesized primer
US-10-120-687-27

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%        Indels:       0
DB:             14          Gaps:         0

US-09-966-880A-8 (1-198) x US-10-120-687-27 (1-20)

QY      59 LeuLeuPheLeuArg 63
|||||
Db      18 TTGCTGTTCTTCGG 4
|||||

RESULT 170
US-10-139-496-35
; Sequence 35, Application US/10139496
; Publication No. US20030082646A1
; GENERAL INFORMATION:
; APPLICANT: Carey, Thomas E.
; APPLICANT: Nair, Thankum S.
; APPLICANT: Gray, Jennifer P.
; TITLE OF INVENTION: Antigenic Targets of Autoimmune Sensorineural Hearing Loss (AISNH
; TITLE OF INVENTION: Development of Tests for Diagnosis and Management of AISNHL
; FILE REFERENCE: UM-6982
; CURRENT APPLICATION NUMBER: US/10/139,496
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/222,179
; PRIOR FILING DATE: 1998-12-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

;
; OTHER INFORMATION: Synthetic
US-10-139-496-35

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%        Indels:       0
DB:             14          Gaps:         0

US-09-966-880A-8 (1-198) x US-10-139-496-35 (1-20)

QY      59 SerPheSerLeuAsp 45
|||||
Db      15 TCCTTCCTCCCTGGAC 1
|||||

RESULT 172
US-10-002-491-62
; Sequence 62, Application US/10002491
; Publication No. US20030109467A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION
; FILE REFERENCE: RTS-0239
; CURRENT APPLICATION NUMBER: US/10/002,491
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

;
; OTHER INFORMATION: Synthetic
US-10-139-496-35

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%        Indels:       0
DB:             14          Gaps:         0

US-09-966-880A-8 (1-198) x US-10-139-496-35 (1-20)

QY      59 GluGlyLeuHisGlu 167
|||||
Db      5 GAGGGTCTCCATGAG 19
|||||

RESULT 171
US-10-181-107-147/c
; Sequence 147, Application US/10181107
; Publication No. US20030083295A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTSP-0325
; CURRENT APPLICATION NUMBER: US/10/181,107
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: PCT/US01/00888
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/484,617
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-107-147

Alignment Scores:
Pred. No.:      4.3e+03      Length:      20
Score:          5.00        Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    2.53%        Indels:       0
DB:             14          Gaps:         0

US-09-966-880A-8 (1-198) x US-10-181-107-147 (1-20)

QY      41 SerPheSerLeuAsp 45
|||||
Db      15 TCCTTCCTCCCTGGAC 1
|||||
```



```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-002-491-62

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-002-491-62 (1-20)

QY 8 ArgArgLysPheIeu 12
   |||||
Db 5 AGACGGAGTTCCTT 19

RESULT 173
US-10-295-942-56
; Sequence 56, Application US/10295942
; Publication No. US20030109480A1
; GENERAL INFORMATION:
; APPLICANT: Cordex, Roger
; APPLICANT: Smith, Adrian
; APPLICANT: Higenbottom, Tim
; APPLICANT: Rothblatt, Martine
; APPLICANT: Vane, John
; APPLICANT: Jones, Delphine
; TITLE OF INVENTION: INHIBITORS OF ENDOTHELIN-1 SYNTHESIS
; FILE REFERENCE: 080618/0123
; CURRENT APPLICATION NUMBER: US/10/295,942
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/527,240
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ASON
US-10-295-942-56

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-295-942-56 (1-20)

QY 23 GlyArgArgLuthr 27
   |||||
Db 2 GGGCGTCGGCAACT 16

RESULT 174
US-10-173-225B-71
; Sequence 71, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPR-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961

; OTHER INFORMATION: Description of Artificial Sequence:
US-10-265-689-19

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-265-689-19 (1-20)

; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-173-225B-71

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-173-225B-71 (1-20)

QY 169 SerValArgLeuSer 173
   |||||
Db 4 TCCTGAGGCTTCA 18

RESULT 175
US-10-265-689-19
; Sequence 19, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-265-689-19

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-265-689-19 (1-20)
```

QY 22 LysGlyArgGlu 26
 |||||
 DB 5 AAGGGAAGGCGAA 19

RESULT 176

US-10-265-689-30
 ; Sequence 30, Application US/10265689
 ; Publication No. US2003011975A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SURMIT, RICHARD S.
 ; APPLICANT: COLLINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL F.
 ; APPLICANT: RICQUIER, DANIEL
 ; APPLICANT: BOULLAUD, FREDERIC
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
 ; FILE REFERENCE: 1579-376
 ; CURRENT APPLICATION NUMBER: US/10/265,689
 ; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/353,645
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864
 ; PRIOR FILING DATE: 1997-04-22
 ; PRIOR APPLICATION NUMBER: 60/034,960
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-10-265-689-30

Alignment Scores:
 Pred. No.: 20
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Query Match: 2.53%
 Indels: 0
 DB: 14
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-265-689-30 (1-20)

QY 22 LysGlyArgGlu 26
 |||||
 DB 5 AAGGGAAGGCGAA 19

RESULT 177

US-10-000-213-58
 ; Sequence 58, Application US/10000213
 ; Publication No. US20030125271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker
 ; APPLICANT: Mark P. Roach
 ; APPLICANT: Kenneth Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF VITAMIN D NUCLEAR RECEPTOR EXPRESSION
 ; FILE REFERENCE: RTS-0327
 ; CURRENT APPLICATION NUMBER: US/10/000,213
 ; CURRENT FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 94
 ; SEQ ID NO 58
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-000-213-58

Alignment Scores:
 Pred. No.: 20
 Length: 20

Score: 5.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 14
 Matches: 5
 Conservatives: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-000-213-58 (1-20)

QY 70 LeuAspProGlyArg 74
 |||||
 DB 5 TTAGACCAGGCGCA 19

RESULT 178

US-10-339-604-31
 ; Sequence 31, Application US/10339604
 ; Publication No. US20030152982A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DE BEENHOUWER, HANS
 ; APPLICANT: FORTAELS, FRANCOISE
 ; APPLICANT: NACHTELINCKX, LIEVE
 ; APPLICANT: JANNES, GEERT
 ; APPLICANT: ROSSAU, RUDI
 ; TITLE OF INVENTION: Oligonucleotide Molecules for Use in Detection of Mycobacterium
 ; FILE REFERENCE: 1657.0010001
 ; CURRENT APPLICATION NUMBER: US/10/339,604
 ; CURRENT FILING DATE: 2003-01-10
 ; PRIOR APPLICATION NUMBER: US/09/722,319
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 08/750,088
 ; PRIOR FILING DATE: 1996-12-06
 ; PRIOR APPLICATION NUMBER: PCT/EP95/02230
 ; PRIOR FILING DATE: 1995-06-09
 ; PRIOR APPLICATION NUMBER: EP 94870093.5
 ; PRIOR FILING DATE: 1994-06-09
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-10-339-604-31

Alignment Scores:
 Pred. No.: 20
 Score: 5.00
 Matches: 5
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.53%
 DB: 14
 Matches: 5
 Conservatives: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-339-604-31 (1-20)

QY 92 ArgHisValAlaAsp 96
 |||||
 DB 4 CGGCATGTCGGAT 18

RESULT 179

US-10-037-986-59
 ; Sequence 59, Application US/10037986
 ; Publication No. US20030157487A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Larry Gold
 ; APPLICANT: Craig Tuerk
 ; TITLE OF INVENTION: Nucleic Acid Ligands
 ; NUMBER OF SEQUENCES: 374
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado

COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/CT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-037-986-59
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-037-986-59 (1-20)
QY 32 ValVallveARG 36
Db 4 GTGTAAACGACGG 18
RESULT 180
US-10-037-066-7/c
Sequence 7, Application US/10371066
Publication No. US20030162214A1
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
MICROELECTRONIC SYSTEMS AND DEVICES FOR
DIAGNOSTICS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/371,066
FILING DATE: 21-Feb-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/146,504
FILING DATE: No. US20030162214A1ember 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-371-066-7
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-371-066-7 (1-20)
QY 56 HisValGluLeu 60
Db 18 CACGTAGAACTGCTC 4
RESULT 181
US-10-133-779-78/c
Sequence 78, Application US/10133779
Publication No. US20030165894A1
GENERAL INFORMATION:
APPLICANT: Chow, Robert
APPLICANT: Tonai, Richard
APPLICANT: StemCyt, Inc
TITLE OF INVENTION: High Throughput Methods of HLA Typing
FILE REFERENCE: 020035-000210US
CURRENT APPLICATION NUMBER: US/10/133,779
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/747,391
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/172,768
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Fast-Seq for Windows Version 3.0
SEQ ID NO 78
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-133-779-78
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0

```
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-133-779-78 (1-20)
QY 112 ArgLeuTyPheCys 116
DB 20 GCCTGTGACTTCTGT 6

RESULT 182
US-10-218-969-92
; Sequence 92, Application US/10218969
; Publication No. US20030165916A1
; GENERAL INFORMATION:
; APPLICANT: Sealfon, Stuart
; APPLICANT: Yuen, Tony
; APPLICANT: Wurmbach, Elisa
; TITLE OF INVENTION: Use of Intrinsic Reporters of Cell Signaling For High Content Drug
; TITLE OF INVENTION: Profiling and Toxicity Screening
; FILE REFERENCE: 2459-1-007N
; CURRENT APPLICATION NUMBER: US/10/218,969
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/312,220
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/324,895
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-969-92

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-218-969-92 (1-20)
QY 94 ValAlaAspPheLeu 98
DB 6 GTGCTGACTTCTGT 20

RESULT 183
US-10-388-307-11/c
; Sequence 11, Application US/10388307
; Publication No. US20030180778A1
; GENERAL INFORMATION:
; APPLICANT: Schwientek, Tilo
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: UPD-N-Acetylglucosamine:
; TITLE OF INVENTION: Galactose-beta1,3-N-Acetylglactosamine-alpha-R / (GlcNAc
; TITLE OF INVENTION: to GalNAc) beta1,6-N-Acetylglucosaminyltransferase, C2GnT3
; FILE REFERENCE: 4503/1G031
; CURRENT APPLICATION NUMBER: US/10/388,307
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US/09/645,192
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/150,488
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-388-307-11
```

```
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
```

US-09-966-880A-8 (1-198) x US-10-388-307-11 (1-20)

```
QY 125 GlyLeuArgArgLeu 129
DB 18 GGGTTGAGGAGACTG 4
```

RESULT 184

```
US-10-419-341-16
; Sequence 16, Application US/10419341
; Publication No. US20030180785A1
; GENERAL INFORMATION:
; APPLICANT: Krishnan, Rajendra
; APPLICANT: Coleman, Rebecca A.
; APPLICANT: Yoder, Christine C.
; APPLICANT: Dartschi, Becky A.
; APPLICANT: Brake, David
; TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULES ENCODING NEOSPORA PROTEINS
; FILE REFERENCE: PC9943A
; CURRENT APPLICATION NUMBER: US/10/419,341
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/276,438
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/079,389
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/112,282
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Neospora caninum
US-10-419-341-16
```

```
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0
```

US-09-966-880A-8 (1-198) x US-10-419-341-16 (1-20)

```
QY 39 AlaThrSerPheSer 43
DB 4 GCGACTTCTTTTCT 18
```

RESULT 185

```
US-10-032-585-4132/c
; Sequence 4132, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4132
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4132

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-032-585-4132 (1-20)
QY 22 LysGlyArgGlu 26
Db 19 AAGGCGAGGGGAA 5

RESULT 186
US-10-032-585-5401/c
; Sequence 5401, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 0182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5401
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5401

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-032-585-5401 (1-20)
QY 43 SerLeuArgPheGly 47
Db 16 AGCCITGACTCGGG 2

RESULT 187
US-10-109-349A-8
; Sequence 8, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REA
; TITLE OF INVENTION: METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL SAM
; FILE REFERENCE: 01154/2001-203
; CURRENT APPLICATION NUMBER: US/10/109,349A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-10-109-349A-8

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-109-349A-8 (1-20)
QY 38 SerAlaThrSerPhe 42
Db 1 TCAGCAACCTCTTTC 15

RESULT 188
US-10-109-349A-262
; Sequence 262, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN R
; TITLE OF INVENTION: METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL S
; FILE REFERENCE: 01154/2001-203
; CURRENT APPLICATION NUMBER: US/10/109,349A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-109-349A-262

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-109-349A-262 (1-20)
QY 19 ArgTTPAlaLysGly 23
Db 1 AGGTGGGCAAGGGA 15

RESULT 189
US-10-170-172-7/c
; Sequence 7, Application US/10170172
; Publication No. US20030190632A1
; GENERAL INFORMATION:
; APPLICANT: SOSNOWSKI, RONALD G
; APPLICANT: BUTLER, WILLIAM F
; APPLICANT: TU, EUGENE
; APPLICANT: NERENBERG, MICHAEL I
; APPLICANT: HELLER, MICHAEL J
; APPLICANT: EDMAN, CARL F
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING MICROELECTRONIC
; TITLE OF INVENTION: INTEGRATED SYSTEMS, COMPONENT DEVICES, MECHANISMS,
; TITLE OF INVENTION: METHODS, AND PROCEDURES FOR MOLECULAR BIOLOGICAL
; TITLE OF INVENTION: ANALYSIS AND DIAGNOSTICS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 227/194
; CURRENT APPLICATION NUMBER: US/10/170,172
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US/08/986,065
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: tRNA
LOCATION: (20)
OTHER INFORMATION: Synthesized with U at 3' terminus to provide
OTHER INFORMATION: ribonucleic acid base for reactivity
US-10-170-172-7

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-170-172-7 (1-20)
QY 56 HisValGluLeu 60
DB 18 CACGTAGACTGCTC 4

RESULT 190
US-10-408-085-59
Sequence 59, Application US/10408085
Publication No. US20030198989A1
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/408,085
FILING DATE: 03-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-408-085-59

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-408-085-59 (1-20)
QY 32 ValVallyeArgArg 36
DB 4 GTTGTAAACGACGG 18

RESULT 191
US-10-380-931-5
Sequence 5, Application US/10380931
Publication No. US20030215944A1
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
APPLICANT: Susan M. Freier
TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTSP-0187
CURRENT APPLICATION NUMBER: US/10/380,931
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: 09/676,610
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-931-5

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-380-931-5 (1-20)
QY 129 LeuHisArgAlaGly 133
DB 6 TTGCACAGGCGCAGG 20

RESULT 192
US-10-126-685-104/c
Sequence 104, Application US/10126685
Publication No. US20030219722A1
GENERAL INFORMATION:
APPLICANT: Ladner, Robert Charles
Guterman, Sonia Kosow
Roberts, Bruce Lindsay
Markland, William
Ley, Arthur Charles
Kent, Rachel Baribault
TITLE OF INVENTION: Directed Evolution of No. US20030219722A1e1

; Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Broadway and Neimark
; STREET: 419 Seventh Street, N.W.
; Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/126,685
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,319
; FILING DATE: 1993-01-26
; APPLICATION NUMBER: 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-126-685-104

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-126-685-104 (1-20)
QY 178 ArgilleLeuPro 182
Db 18 CGGATCCTCCTCCCT 4

RESULT 193
US-10-236-031B-89/c
; Sequence 89, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236,031B

; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,389
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-236-031B-89

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-236-031B-89 (1-20)
QY 117 GluAspArgLysala 121
Db 17 GAAGACCGAAGGCT 3

RESULT 194
US-10-174-771-30/c
; Sequence 30, Application US/10174771
; Publication No. US2003023034A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF JUNCTIONAL ADHESION MOLECULE 3 EXPRESSI
; FILE REFERENCE: RTS-0430
; CURRENT APPLICATION NUMBER: US/10/174,771
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 151
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-771-30

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-771-30 (1-20)
QY 35 ArgArgAspSerAla 39
Db 17 CGGAGAGACTCAGCC 3

RESULT 195
US-10-174-771-101
; Sequence 101, Application US/10174771
; Publication No. US2003023034A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF JUNCTIONAL ADHESION MOLECULE 3 EXPRESSI
; FILE REFERENCE: RTS-0430
; CURRENT APPLICATION NUMBER: US/10/174,771
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 151
; SEQ ID NO 101
; LENGTH: 20

; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-174-771-101

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-771-101 (1-20)

QY 35 ArgArgAspSerAla 39

Db 4 CGGAGAGACTCAGCC 18

RESULT 196

; Sequence 33, Application US/10176277
; Publication No. US20030232443A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION
; FILE REFERENCE: HTS-0022
; CURRENT APPLICATION NUMBER: US/10/176,277
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-176-277-33

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-176-277-33 (1-20)

QY 35 ArgArgAspSerAla 39

Db 1 CGGCGAGACTCTGCA 15

RESULT 197

; Sequence 65, Application US/10176277
; Publication No. US20030232443A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CENTROMERE PROTEIN B EXPRESSION
; FILE REFERENCE: HTS-0022
; CURRENT APPLICATION NUMBER: US/10/176,277
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-176-277-65

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-176-277-65 (1-20)

QY 35 ArgArgAspSerAla 39

Db 20 CGGCGAGACTCTGCA 6

RESULT 198

; Sequence 25, Application US/10174559
; Publication No. US20030232773A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DRAK1 EXPRESSION
; FILE REFERENCE: PTS-0006
; CURRENT APPLICATION NUMBER: US/10/174,559
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 112
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-174-559-25

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-174-559-25 (1-20)

QY 40 ThrSerPheSerIeu 44

Db 3 ACATCTTTTCTTTA 17

RESULT 199

; Sequence 104, Application US/10127028
; Publication No. US20040005539A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. US20040005539A1el
; Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,028
FILING DATE: 22-APR-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/009,319
FILING DATE: 1993-01-26
APPLICATION NUMBER: 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-127-028-104

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-127-028-104 (1-20)

QY 178 ArgilleLeuLeupro 182
DB 18 CGGATCCCTCCCT 4

RESULT 200

US-10-190-366-185/c
Sequence 185, Application US/10190366
Publication No. US20040006031A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REFERENCE: PTS-0023
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 409
SEQ ID NO 185
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-185

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-190-366-185 (1-20)

QY 78 ValThrTrpPheThr 82
DB 20 GTCACATGGTTCACA 6

RESULT 201

US-10-190-366-378
Sequence 378, Application US/10190366
Publication No. US20040006031A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
FILE REFERENCE: PTS-0023
CURRENT APPLICATION NUMBER: US/10/190,366
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 409
SEQ ID NO 378
LENGTH: 20
TYPE: DNA
ORGANISM: M. musculus
FEATURE:
US-10-190-366-378

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-190-366-378 (1-20)

QY 78 ValThrTrpPheThr 82
DB 1 GTCACATGGTTCACA 15

RESULT 202

US-10-289-762-3206/c
Sequence 3206, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
of thereof and uses thereof, in particular for the diagnosis, pre
treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 3206
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-10-289-762-3206

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-3206 (1-20)

QY 169 SerValArgLeuSer 173
 Db 19 TCCGTGAGACTCTCT 5

RESULT 203

US-10-289-762-3704/c

; Sequence 3704, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3704

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-3704

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-3704 (1-20)

QY 103 AsnLeuSerLeuArg 107

Db 20 AACCTCTCTCTGAGG 6

RESULT 204

US-10-289-762-3731/c

; Sequence 3731, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3731

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-3731

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-3731 (1-20)

QY 104 LeuSerLeuArgIle 108

Db 16 TTGTCTCTGAGATC 2

RESULT 205

US-10-289-762-3975

; Sequence 3975, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3975

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-3975

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-3975 (1-20)

QY 176 LeuArgArgIleLeu 180

Db 6 TTGAGGAGGATCCTG 20

RESULT 206

US-10-289-762-4543

; Sequence 4543, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4543

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-4543

Alignment Scores:

Pred. No.:	4.3e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-289-762-4543 (1-20)

QY 111 AlaArgLeuTyrPhe 115

Db 2 GCCAGGCTGTATTTC 16

RESULT 207

US-10-289-762-4632/c

; Sequence 4632, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4632

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-4632

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-4632 (1-20)

QY 179 IleLeuLeuProLeu 183

DB 20 ATTCTACTCCCTCTC 6

RESULT 208

US-10-289-762-4660/c

; Sequence 4660, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4660

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-4660

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-4660 (1-20)

QY 40 ThrSerPheSerLeu 44

DB 18 ACATCGTCTCCCTA 4

RESULT 209

US-10-289-762-5412/c

; Sequence 5412, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5412

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-5412

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-5412 (1-20)

QY 126 LeuArgLeuHis 130

DB 17 CTAAGCGGCTTACAT 3

RESULT 210

US-10-289-762-5709/c

; Sequence 5709, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 5709

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-5709

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-5709 (1-20)

QY 104 LeuSerLeuArgile 108

DB 15 CTGCTCTCCGCATA 1

RESULT 211

US-10-289-762-6382/c

; Sequence 6382, Application US/10289762

; Publication No. US20040006218A1

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; FILE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/10/289,762

; CURRENT FILING DATE: 2003-03-27

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 6382

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-10-289-762-6382

Alignment Scores:

Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-6382 (1-20)

Qy 58 GluLeuPheLeu 62
DB 20 GAGCTTCTCTTTTA 6

RESULT 212

US-10-289-762-6501

; Sequence 6501, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

US-10-289-762-6501

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-289-762-6501 (1-20)

Qy 41 SerPheSerLeuAsp 45

DB 5 AGTTTCTCTAGAC 19

RESULT 213

US-10-188-777-88/C

; Sequence 88, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0358
; CURRENT APPLICATION NUMBER: US/10/188,777
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-777-88

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-777-88 (1-20)

Qy 170 ValArgLeuSerArg 174

DB 16 GTCCGCTCAGTCGC 2

RESULT 214

US-10-188-777-137

; Sequence 137, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0358
; CURRENT APPLICATION NUMBER: US/10/188,777
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens

US-10-188-777-137

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-188-777-137 (1-20)

Qy 170 ValArgLeuSerArg 174

DB 5 GTCCGCTCAGTCGC 19

RESULT 215

US-10-397-635-1

; Sequence 1, Application US/10397635
; Publication No. US2004000604A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, XIAOLI
; APPLICANT: FU, XUPING
; TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
; FILE REFERENCE: P02410US2
; CURRENT APPLICATION NUMBER: US/10/397,635
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,788
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/410,024
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-397-635-1

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-397-635-1 (1-20)

QY 94 ValAlaAspPheLeu 98
Db 5 GTTGGGACTTCTG 19

RESULT 216
US-10-126-544-104/c
; Sequence 104, Application US/10126544
; Publication No. US20040023205A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; Guterman, Sonia Kosow
; Roberts, Bruce Lindsay
; Markland, William
; Ley, Arthur Charles
; Kent, Rachel Barbault
; TITLE OF INVENTION: Directed Evolution of No. US20040023205A1e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brodsky and Neimark
; STREET: 419 Seventh Street, N.W.
; Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/126,544
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/009,319
; FILING DATE: 1993-01-26
; APPLICATION NUMBER: 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-126-544-104

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-126-544-104 (1-20)

QY 178 ArgIleIeuLeuPro 182
Db 18 CGGATCCTCCTCCCT 4

RESULT 217
US-10-210-479-21
; Sequence 21, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-21
Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-210-479-21 (1-20)

QY 173 SerArgGlnLeuArg 177
Db 6 AGCCGACAGCTCGA 20

RESULT 218
US-10-210-556-50/c
; Sequence 50, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-556-50

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-210-556-50 (1-20)

QY 82 ThrSerTrpSerPro 86
Db 19 ACCTCCTGCTCACC 5

```
RESULT 219
US-10-210-556-173
; Sequence 173, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTTPA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 173
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-210-556-173

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-210-556-173 (1-20)

QY 82 ThrSerTrpSerPro 86
| | | | | | | | | |
DB 2 ACCTCTGTCACCA 16

RESULT 220
US-10-363-198-16
; Sequence 16, Application US/10363198
; Publication No. US20040023908A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/10/363,198
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 09/658,687
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-363-198-16

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-363-198-16 (1-20)

QY 107 ArgIlePheThrAla 111
| | | | | | | | | |
DB 1 CGTATCTTCACAGCT 15

RESULT 221
US-10-444-206-69
; Sequence 69, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-69

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-206-69 (1-20)

QY 176 LeuArgArgIleIeu 180
| | | | | | | | | |
DB 1 CTGCGCCGAATCCTG 15

RESULT 222
US-10-444-206-166
; Sequence 166, Application US/10444206
; Publication No. US20040023917A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/10/444,206
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: 09/851,871
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996 12 31
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-444-206-166
```

Alignment Scores:
Pred. No.: 4.3e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-206-166 (1-20)

QY 176 LeuArgArgIleLeu 180
|||||
Db 2 CTGCGCGAATCTTG 16

RESULT 223
US-09-837-344-39/c
; Sequence 39, Application US/09837344
; Patent No. US20020041882A1
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,344
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 39: -
US-09-837-344-39

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-444-206-166 (1-20)

QY 176 LeuArgArgIleLeu 180
|||||
Db 2 CTGCGCGAATCTTG 16

RESULT 224
US-09-837-344-43/c
; Sequence 43, Application US/09837344
; Patent No. US20020041882A1
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,344
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,625
; FILING DATE: <Unknown>
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-837-344-43

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-837-344-43 (1-12)

QY 59 LeuLeupheLeu 62
|||||
Db 12 TTGTTGTTCTTG 1

```
RESULT 225
US-09-835-370-54
; Sequence 54, Application US/09835370
; Publication No. US20030022172A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: base sequence of pna derivatives that bind to
; OTHER INFORMATION: viral and cellular targets
US-09-835-370-54

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-835-370-54 (1-12)

QY 82 ThrSerTrpSer 85
Db 1 ACATCATGCTCG 12

RESULT 226
US-09-875-453-18
; Sequence 18, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135.30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-09-875-453-18

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
```

```
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-875-453-18 (1-12)

QY 194 ArgThrLeuGly 197
Db 1 AGGACTCTTGGA 12

RESULT 227
US-09-900-112-56/c
; Sequence 56, Application US/09900112
; Publication No. US20030082209A1
; GENERAL INFORMATION:
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Schmidt, Alexander C.
; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vacci
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Parainfluenza Virus
US-09-900-112-56

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-900-112-56 (1-12)

QY 169 SerValArgLeu 172
Db 12 TCCGTACGTCCTT 1

RESULT 228
US-09-900-112-60/c
; Sequence 60, Application US/09900112
; Publication No. US20030082209A1
; GENERAL INFORMATION:
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Schmidt, Alexander C.
; TITLE OF INVENTION: Attenuated Human-Bovine Chimeric Parainfluenza Virus (PIV) Vacci
; FILE REFERENCE: NIH-0127
; CURRENT APPLICATION NUMBER: US/09/900,112
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/215,809
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```


OTHER INFORMATION: Parainfluenza Virus
US-09-900-112-60

Alignment Scores:
Pred. No.: 12
Score: 3.07e+04 Length: 12
Matches: 4
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.02%
DB: 10
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-900-112-60 (1-12)

QY 169 SerValArgLeu 172
DB 12 TCCGTACGTCTA 1

RESULT 229

US-09-093-972C-852/c
; Sequence 852, Application US/0903972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nvce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOINSTRUCTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 852:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 852:
US-09-093-972C-852

Alignment Scores:
Pred. No.: 12
Score: 3.07e+04 Length: 12
Matches: 4

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.02%
DB: 10
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-852 (1-12)

QY 90 CysAlaArgHis 93
DB 12 TGTGCCCGCAT 1

RESULT 230

US-09-793-146-38
; Sequence 38, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-38

Alignment Scores:
Pred. No.: 12
Score: 3.07e+04 Length: 12
Matches: 4
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.02%
DB: 11
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-793-146-38 (1-12)

QY 82 ThrSerTrpSer 85
DB 1 ACATCATGTCG 12

RESULT 231

US-09-793-146-48
; Sequence 48, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-49

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-793-146-48 (1-12)

Qy 82 ThrSerTrpSer 85
| | | | | | | | | |
Db 1 ACATCATGTCG 12

RESULT 232
US-09-793-146-49/c
; Sequence 49, Application US/09793146
; Publication No. US20030203359A1
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; FILE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-49

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 11 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-793-146-49 (1-12)

Qy 82 ThrSerTrpSer 85
| | | | | | | | | |
Db 12 ACATCATGTCG 1

RESULT 233
US-10-193-451A-24
; Sequence 24, Application US/10193451A
; Publication No. US20030096269A1
; GENERAL INFORMATION:
; APPLICANT: CULLIS, CHRISTOPHER A.
; APPLICANT: RADEMAN, SAMANTHA
; APPLICANT: KUNERT, KARL
; TITLE OF INVENTION: METHOD FOR FINDING GENETIC MARKERS
; FILE REFERENCE: 028315600005
; CURRENT APPLICATION NUMBER: US/10/193,451A
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/292,646
; PRIOR FILING DATE: 1999-04-15
```

```
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: WordPerfect for Windows v. 7.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
US-10-193-451A-24

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-193-451A-24 (1-12)

Qy 41 SerPheSerLeu 44
| | | | | | | | | |
Db 1 AGCTTCTCCCTC 12

RESULT 234
US-10-437-038-24
; Sequence 24, Application US/10437038
; Publication No. US20030228665A1
; GENERAL INFORMATION:
; APPLICANT: GAUTVIK, KAARE M.
; APPLICANT: ALESTROM, PETER
; APPLICANT: OYEN, TORDIS BEATE
; APPLICANT: GABRIELSEN, ODD STOKKE
; TITLE OF INVENTION: PRODUCTION OF HUMAN PARATHYROID HORMONE FROM MICROORGANISMS
; FILE REFERENCE: 016777/0550
; CURRENT APPLICATION NUMBER: US/10/437,038
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US/10/359,091
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 08/463,222
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/340,664
; PRIOR FILING DATE: 1994-11-16
; PRIOR APPLICATION NUMBER: 08/087,471
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 07/821,478
; PRIOR FILING DATE: 1992-01-15
; PRIOR APPLICATION NUMBER: 07/404,970
; PRIOR FILING DATE: 1989-09-08
; PRIOR APPLICATION NUMBER: 07/393,851
; PRIOR FILING DATE: 1989-08-14
; PRIOR APPLICATION NUMBER: 06/921,684
; PRIOR FILING DATE: 1986-10-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-437-038-24

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
```

DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-437-038-24 (1-12)

QY 41 SerPheSerLeu 44
|||||

Db 1 AGCTTCAGCCTC 12

RESULT 235

US-10-359-091-24

Sequence 24, Application US/10359091

Publication No. US20040005668A1

GENERAL INFORMATION:

APPLICANT: GAUTVIK, KAARE M.

APPLICANT: ALESTROM, PETER

APPLICANT: OYEN, TORDIS BEATE

APPLICANT: GABRIELSEN, ODD STOKKE

TITLE OF INVENTION: PRODUCTION OF HUMAN PARATHYROID HORMONE FROM MICROORGANISMS

FILE REFERENCE: 016777/0550

CURRENT APPLICATION NUMBER: US/10/359,091

CURRENT FILING DATE: 2003-02-06

PRIOR APPLICATION NUMBER: 08/463,222

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: 08/340,664

PRIOR FILING DATE: 1994-11-16

PRIOR APPLICATION NUMBER: 08/087,471

PRIOR FILING DATE: 1993-07-02

PRIOR APPLICATION NUMBER: 07/821,478

PRIOR FILING DATE: 1992-01-15

PRIOR APPLICATION NUMBER: 07/404,970

PRIOR FILING DATE: 1989-09-08

PRIOR APPLICATION NUMBER: 07/393,851

PRIOR FILING DATE: 1989-08-14

PRIOR APPLICATION NUMBER: 06/921,684

PRIOR FILING DATE: 1986-10-22

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 24

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide

US-10-359-091-24

Alignment Scores:

Pred. No.:	3.07e-04	Length:	12
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-359-091-24 (1-12)

QY 41 SerPheSerLeu 44
|||||

Db 1 AGCTTCAGCCTC 12

RESULT 236

US-10-422-050-66

Sequence 66, Application US/10422050

Publication No. US20040009510A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Seiwert, Scott

APPLICANT: Zinnen, Shawn

APPLICANT: Vaish, Narendra

APPLICANT: Jadhav, Vasant

APPLICANT: Kossen, Karl

TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

FILE REFERENCE: 700/013 (MEHB 00-816-M)

CURRENT APPLICATION NUMBER: US/10/422,050

CURRENT FILING DATE: 2003-04-23

PRIOR APPLICATION NUMBER: PCT/US 02/35529

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 10/286,492

PRIOR FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: US 10/283,858

PRIOR FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 10/056,761

PRIOR FILING DATE: 2002-01-23

PRIOR APPLICATION NUMBER: US 09/992,160

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 09/877,526

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 09/800,594

PRIOR FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: US 60/187,128

FILE REFERENCE: 700/013 (MEHB 00-816-M)

CURRENT APPLICATION NUMBER: US/10/422,050

CURRENT FILING DATE: 2003-04-23

PRIOR APPLICATION NUMBER: PCT/US 02/35529

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 10/286,492

PRIOR FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: US 10/283,858

PRIOR FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 10/056,761

PRIOR FILING DATE: 2002-01-23

PRIOR APPLICATION NUMBER: US 09/992,160

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 09/877,526

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 09/800,594

PRIOR FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: US 60/187,128

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin version 3.2

SEQ ID NO 66

LENGTH: 12

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule

US-10-422-050-66

Alignment Scores:

Pred. No.:	3.07e-04	Length:	12
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	15	Gaps:	0

US-09-966-880A-8 (1-198) x US-10-422-050-66 (1-12)

QY 100 GlyAsnProAsn 103
|||||

Db 1 GGAAUCCAAAC 12

RESULT 237

US-10-422-050-68

Sequence 68, Application US/10422050

Publication No. US20040009510A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Seiwert, Scott

APPLICANT: Zinnen, Shawn

APPLICANT: Vaish, Narendra

APPLICANT: Jadhav, Vasant

APPLICANT: Kossen, Karl

TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

FILE REFERENCE: 700/013 (MEHB 00-816-M)

CURRENT APPLICATION NUMBER: US/10/422,050

CURRENT FILING DATE: 2003-04-23

PRIOR APPLICATION NUMBER: PCT/US 02/35529

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 10/286,492

PRIOR FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: US 10/283,858

PRIOR FILING DATE: 2002-10-30

PRIOR APPLICATION NUMBER: US 10/056,761

PRIOR FILING DATE: 2002-01-23

PRIOR APPLICATION NUMBER: US 09/992,160

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 09/877,526

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 09/800,594

PRIOR FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: US 60/187,128

FILE REFERENCE: 700/013 (MEHB 00-816-M)

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-68

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-68 (1-12)

Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAAC 12

RESULT 238

US-10-422-050-71
; Sequence 71, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MBHB 00-816-M)
; CURRENT APPLICATION NUMBER: US/10/422,050
; CURRENT FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-71

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-71 (1-12)
Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAAC 12

RESULT 239

US-10-422-050-72
; Sequence 72, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MBHB 00-816-M)
; CURRENT APPLICATION NUMBER: US/10/422,050
; CURRENT FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-72

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-72 (1-12)

Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAAC 12

RESULT 240

US-10-422-050-73
; Sequence 73, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

US-10-422-050-73
; Sequence 73, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules

; FILE REFERENCE: 700/013 (MEHB 00-816-M)
; CURRENT APPLICATION NUMBER: US 10/422,050
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-73

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-73 (1-12)

Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAC 12

RESULT 241
US-10-422-050-74
; Sequence 74, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MEHB 00-816-M)
; CURRENT APPLICATION NUMBER: US 10/422,050
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-75

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-74

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-74 (1-12)

Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAC 12

RESULT 242
US-10-422-050-75
; Sequence 75, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MEHB 00-816-M)
; CURRENT APPLICATION NUMBER: US 10/422,050
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Molecule
US-10-422-050-75

Alignment Scores:
Pred. No.: 3.07e+04 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-422-050-75 (1-12)

Qy 100 GlyAsnProAsn 103
Db 1 GGAAAUCCAAC 12

RESULT 243

US-08-866-279A-13
; Sequence 13, Application US/08866279A
; Publication No. US20020170076A1
; GENERAL INFORMATION:
; APPLICANT: Susan DYMECKI
; TITLE OF INVENTION: Use of Flp Recombinase in Mice
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,279A
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 800
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-866-279A-13

Alignment Scores: Length: 13
Pred. No.: 3.31e+04 Matches: 4
Score: 4.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-08-866-279A-13 (1-13)

Qy 10 LysPheLeuTyr 13
Db 2 AAGTTCCTATAC 13

RESULT 244

US-09-864-785-3628/c
; Sequence 3628, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: 400/022 (MEHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3628
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3628

Alignment Scores: Length: 13
Pred. No.: 3.31e+04 Matches: 4
Score: 4.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-864-785-3628 (1-13)

Qy 72 ProGlyArgCys 75
Db 12 CCAGGAGATGC 1

RESULT 245

US-09-864-785-3657
; Sequence 3657, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: 400/022 (MEHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3657
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-3657

Alignment Scores: Length: 13
Pred. No.: 3.31e+04 Matches: 4
Score: 4.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-864-785-3657 (1-13)

Qy 59 LeuLeuPheLeu 62
Db 2 UUGCUCUCUUA 13

RESULT 246

US-09-093-972C-840/c
; Sequence 840, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nycs, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRUCTION, ALLERGY (IBS) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 840:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 840:
US-09-093-972C-840
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-093-972C-840 (1-13)
QY 90 CysAlaArgHis 93
Db 13 TGTGCCCGCCAT 2
RESULT 247
US-09-093-972C-851/c
; Sequence 851, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 851:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 851:
US-09-093-972C-851
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-093-972C-851 (1-13)
QY 90 CysAlaArgHis 93
Db 12 TGTGCCCGCCAT 1
RESULT 248
US-10-357-567-58/c
; Sequence 58, Application US/10357567
; Publication No. US20040038382A1
; GENERAL INFORMATION:
; APPLICANT: Coehigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-07748
; CURRENT APPLICATION NUMBER: US/10/357,567
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/046,845
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.2
; SEQ ID NO: 58
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-357-567-58
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-357-567-58 (1-13)
QY 195 ThrLeuGlyLeu 198
DB 13 ACACAGGCTG 2
RESULT 249
US-10-005-956-877/c
; Sequence 877, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 877
; LENGTH: 13
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-877
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-005-956-877 (1-13)
QY 39 AlaThrSerPhe 42
DB 12 GCCACGAGCTTC 1
RESULT 250
US-10-005-956-903/c
; Sequence 903, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 903
; LENGTH: 13
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-903
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13

Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-005-956-903 (1-13)
QY 39 AlaThrSerPhe 42
DB 12 GCCACGAGCTTC 1
RESULT 251
US-10-156-433-1
; Sequence 1, Application US/10156433
; Publication No. US20030144489A1
; GENERAL INFORMATION:
; APPLICANT: Burgin, Alex
; APPLICANT: Beigelman, Leonid
; APPLICANT: Bellon, Laurent
; APPLICANT: Zinnen, Shawn
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-943-E (500.007)
; CURRENT APPLICATION NUMBER: US/10/156,433
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/112,814
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-433-1
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-156-433-1 (1-13)
QY 59 LeuLeuPheLeu 62
DB 1 TTGCTTTTCCTC 12
RESULT 252
US-10-156-433-2
; Sequence 2, Application US/10156433
; Publication No. US20030144489A1
; GENERAL INFORMATION:
; APPLICANT: Burgin, Alex
; APPLICANT: Beigelman, Leonid
; APPLICANT: Bellon, Laurent
; APPLICANT: Zinnen, Shawn
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-943-E (500.007)
; CURRENT APPLICATION NUMBER: US/10/156,433
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/112,814

; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-433-2

Alignment Scores:
Pred. No.: 3,31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-433-2 (1-13)

Qy 59 LeuLeuPheLeu 62
Db 2 TTGCTTTCTC 13

RESULT 253
US-10-156-433-13
; Sequence 13, Application US/10156433
; Publication No. US2003014489A1
; GENERAL INFORMATION:
; APPLICANT: Burgin, Alex
; APPLICANT: Beigelman, Leonid
; APPLICANT: Bellon, Laurent
; APPLICANT: Zinnen, Shawn
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MHB00-943-E (500.007)
; CURRENT APPLICATION NUMBER: US/10/156,433
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/112,814
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-433-13

Alignment Scores:
Pred. No.: 3,31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-156-433-13 (1-13)

Qy 70 LeuAspProGly 73
Db 1 CTGGATCCAGGA 12

RESULT 254
US-10-104-025-8/c
; Sequence 8, Application US/10104025
; Publication No. US20030165876A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMA SA
; APPLICANT: BLANCHE, Francis
; APPLICANT: CAMERON, Beatrice
; TITLE OF INVENTION: PROCESSES FOR PURIFYING AND FOR DETECTING TARGET DOUBLE-STRANDED
; FILE REFERENCE: 03806.0546
; CURRENT APPLICATION NUMBER: US/10/104,025
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 60/285,272
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: FR 0103953
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-025-8

Alignment Scores:
Pred. No.: 3,31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-104-025-8 (1-13)

Qy 180 LeuLeuProLeu 183
Db 13 CTTCTTCCTCTT 2

RESULT 255
US-10-112-814-1
; Sequence 1, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bellon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MHB00-943-D; 400.005
; CURRENT APPLICATION NUMBER: US/10/112,814
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-1

```
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-1 (1-13)
QY 59 LeuLeuPheLeu 62
Db 1 TTGCTTTTCCTC 12

RESULT 256
US-10-112-814-2
; Sequence 2, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bailor
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH900-943-D; 400.005
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US/10/112,814
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-2
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-2 (1-13)
QY 59 LeuLeuPheLeu 62
Db 2 TTGCTTTTCCTC 13

RESULT 257
US-10-112-814-13
; Sequence 13, Application US/10112814
; Publication No. US20030170644A1
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bailor
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH900-943-D; 400.005
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US/10/112,814
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-2
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-2 (1-13)
QY 59 LeuLeuPheLeu 62
Db 2 TTGCTTTTCCTC 13

RESULT 258
US-10-190-312A-121
; Sequence 121, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arle P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 121
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FRT sequence
US-10-190-312A-121
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-190-312A-121 (1-13)
QY 10 LysPheLeuTyr 13
Db 2 AAGTTCTATAC 13

RESULT 259
US-10-148-521-15/c
```

```
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-10-112-814-13
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-112-814-13 (1-13)
QY 70 LeuAspProGly 73
Db 1 CTGGATCCAGGA 12

RESULT 258
US-10-190-312A-121
; Sequence 121, Application US/10190312A
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Otte, Arle P.
; APPLICANT: Kruckeberg, Arthur L.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; FILE REFERENCE: 2183-4993.1
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US/10/190,312A
; PRIOR FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 1079
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 121
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FRT sequence
US-10-190-312A-121
Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-190-312A-121 (1-13)
QY 10 LysPheLeuTyr 13
Db 2 AAGTTCTATAC 13

RESULT 259
US-10-148-521-15/c
```

; Sequence 15, Application US/10148521
; Publication No. US20030221203A1
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh
; APPLICANT: Lotze, Michael T.
; APPLICANT: Agha-Mohammadi, Siamak T.
; TITLE OF INVENTION: High Efficiency Regulatable Gene Expression System
; FILE REFERENCE: 00791PCT
; CURRENT APPLICATION NUMBER: US/10/148,521
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/237,633
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic linker forward oligonucleotide
US-10-148-521-15

Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-148-521-15 (1-13)

QY 188 AspLeuAcArg 191
Db 12 GACCTTAGGAC 1

RESULT 260
US-10-194-180A-6
; Sequence 6, Application US/10194180A
; Publication No. US20040009179A1
; GENERAL INFORMATION:
; APPLICANT: Kleven, Stanley H.
; APPLICANT: Ferguson, Naola
; TITLE OF INVENTION: Mycoplasma gallisepticum Formulation
; FILE REFERENCE: 1700-002
; CURRENT APPLICATION NUMBER: US/10/194,180A
; CURRENT FILING DATE: 2002-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Mycoplasma gallisepticum
US-10-194-180A-6

Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-194-180A-6 (1-13)

QY 33 ValIysArg 36
Db 1 GTAAACGCGG 12

RESULT 261
US-10-271-429A-4/c
; Sequence 4, Application US/10271429A
; Publication No. US20040023233A1

; GENERAL INFORMATION:
; APPLICANT: Atherogenics, Inc.
; TITLE OF INVENTION: Protection Against Oxidative Stress and Inflammation by a Cytoc
; TITLE OF INVENTION: Response Element
; FILE REFERENCE: ATH118
; CURRENT APPLICATION NUMBER: US/10/271,429A
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: human
US-10-271-429A-4

Alignment Scores:
Pred. No.: 3.31e+04 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 16 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-271-429A-4 (1-13)

QY 38 SerAlaThrSer 41
Db 13 TCTGCCACCTCA 2

RESULT 262
US-08-591-486B-32
; Sequence 32, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Gottingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Trea
; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-9350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-591-486B-32

Alignment Scores:
Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-08-591-486B-32 (1-14)

QY 125 GlyLeuArgGag 128
|||||
DB 2 GGTGGCGTAGA 13

RESULT 263

US-09-504-231A-1373/C
Sequence 1373, Application US/09504231A

Patent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth

APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 09/274,553

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1373

LENGTH: 14

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1373

Alignment Scores:
Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-504-231A-1373 (1-14)

QY 155 HisGluArgThr 158
|||||
DB 12 CATGACGCGACC 1

RESULT 264

US-09-504-231A-1375

Sequence 1375, Application US/09504231A

Patent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth

APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 09/274,553

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1375

LENGTH: 14

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1375

Alignment Scores:

Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Conservative: 0
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-504-231A-1375 (1-14)

QY 110 ThrAlaArgLeu 113
|||||
DB 3 ACUGCCCGUCUC 14

RESULT 265

US-09-504-231A-1411

Sequence 1411, Application US/09504231A

Patent No. US20020013458A1

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth

APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

FILE REFERENCE: rpi 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 09/274,553

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1411
; LENGTH: 14
; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1411

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-504-231A-1411 (1-14)

QY 42 PheSerLeuApp 45

Db 2 UUCAGCUUGGAU 13

RESULT 266

US-09-504-231A-1469

; Sequence 1469, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; FILE REFERENCE: rpi 247/282

; CURRENT FILING DATE: 1999-03-23

; CURRENT APPLICATION NUMBER: US/09/504,231A

; PRIOR FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1469

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-1469

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-504-231A-1469 (1-14)

QY 174 ArgGlnLeuArg 177

Db 1 CGGCGACUCCGG 12

RESULT 267

US-09-804-700-8

; Sequence 8, Application US/09804700

; Patent No. US20020081594A1

; GENERAL INFORMATION:

; APPLICANT: Ladner, Robert D.

; APPLICANT: Caradonna, Salvatore J.

; TITLE OF INVENTION: Uracil DNA Metabolism As A Target For Chemotherapy:

; TITLE OF INVENTION: Screening Assays and Related Method

; FILE REFERENCE: UMDNJ SOM-00-06

; CURRENT APPLICATION NUMBER: US/09/804,700

; CURRENT FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: US 60/189,516

; PRIOR FILING DATE: 2000-03-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 14

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Saccharomyces cerevisiae synthetic oligonucleotide

US-09-804-700-8

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-804-700-8 (1-14)

QY 128 ArgLeuHisArg 131

Db 2 CGCCTCCACCGC 13

RESULT 268

US-09-274-553D-1373/c

; Sequence 1373, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; FILE REFERENCE: rpi 247/282

; CURRENT FILING DATE: 1999-03-23

; CURRENT APPLICATION NUMBER: US/09/274,553D

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1373

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-1373

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-274-553D-1373 (1-14)

QY 155 HisGluArgThr 158
| | | | |
Db 12 CATGAGCGGACC 1

RESULT 269

US-09-274-553D-1375

; Sequence 1375, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1375

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-1375

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-274-553D-1375 (1-14)

QY 110 ThrAlaArgLeu 113
| | | | |
Db 3 ACUGCCGUCUC 14

RESULT 270

US-09-274-553D-1411

; Sequence 1411, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1411
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1411

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-274-553D-1411 (1-14)

QY 42 PheSerLeuArg 45
| | | | |
Db 2 UUCAGCUCUGAU 13

RESULT 271

US-09-274-553D-1469

; Sequence 1469, Application US/09274553D

; Patent No. US2002008225A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: rpi 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1469

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-1469

Alignment Scores:

Pred. No.:	3.54e+04	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-274-553D-1469 (1-14)

QY 174 ArgGlnLeuArg 177
| | | | |
Db 1 CGGCAGCUCGCG 12

RESULT 272

US-09-931-184-1

; Sequence 1, Application US/09931184

; Patent No. US20020119095A1

; GENERAL INFORMATION:

APPLICANT: Gabathuler, Reinhard
APPLICANT: Kolaitis, Gerrassimos
APPLICANT: Brooks, Robert
APPLICANT: Chen, Qingqi
APPLICANT: Karkan, Delara
APPLICANT: Arthur, Gavin
APPLICANT: St. Pierre, Jean Paul
APPLICANT: Jeffries, Wilfred
APPLICANT: Vitalis, Timothy
TITLE OF INVENTION: Chemotherapeutic Agents Conjugated to p97 and Their Methods of Use
FILE REFERENCE: 7685-47
CURRENT APPLICATION NUMBER: US/09/931,184
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/226,254
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-931-184-1

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-931-184-1 (1-14)

Qy 95 AlaAspPheLeu 98
Db 1 GCGGACTTCCTC 12

RESULT 273
US-09-915-063-2/c
Sequence 2, Application US/09915063
Publication No. US20030082544A1
GENERAL INFORMATION:
APPLICANT: Fors, Lance
APPLICANT: Ganske, Rocky
TITLE OF INVENTION: Methods and Systems for Validating Detection Assays, Developing I
TITLE OF INVENTION: Diagnostic DNA or RNA Analysis Products, and Increasing Revenue
TITLE OF INVENTION: Margins from In-Vitro Diagnostic DNA or RNA Analysis Assays
FILE REFERENCE: FORS-06467
CURRENT APPLICATION NUMBER: US/09/915,063
CURRENT FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: 60/304,521
PRIOR FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-915-063-2

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-931-184-1 (1-14)

Qy 95 AlaAspPheLeu 98
Db 1 GCGGACTTCCTC 12

US-09-966-880A-8 (1-198) x US-09-915-063-2 (1-14)

Qy 38 SerAlaThrSer 41
Db 13 TCTGCCACGTCA 2

RESULT 274
US-09-972C-827/c
Sequence 827, Application US/09093972C
Publication No. US20030087845A1
GENERAL INFORMATION:
APPLICANT: Nyce, Jonathan W.
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHIOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 827:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 827:
US-09-931-972C-827

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-931-972C-827 (1-14)

Qy 90 CysAlaArgHis 93
Db 14 TGTGCCCGCAT 3

RESULT 275

US-09-093-972C-839/c
; Sequence 839, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-June-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 839:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 839:
US-09-093-972C-839

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-839 (1-14)

Qy 90 CysAlaArgHis 93

Db 13 TGTGCCCGCCAT 2

RESULT 276

US-09-972C-850/c
; Sequence 850, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.

; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION

NUMBER OF SEQUENCES: 996
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: New Jersey
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,972C
FILING DATE: 09-June-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 08/757,024
FILING DATE: 26-11-1996
APPLICATION NUMBER: US 08/472,527
FILING DATE: 7-June-1995
APPLICATION NUMBER: US 09/016,464
FILING DATE: 30-January-1998

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00672
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 850:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 850:
US-09-093-972C-850

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-093-972C-850 (1-14)

Qy 90 CysAlaArgHis 93

Db 12 TGTGCCCGCCAT 1

RESULT 277

US-09-929-135-2/c
; Sequence 2, Application US/09929135
; Publication No. US20030104470A1
; GENERAL INFORMATION:
; APPLICANT: Fors, Lance
; APPLICANT: Ganske, Rocky
; APPLICANT: Brower, Amy M.
; APPLICANT: Ziarno, Witold M.
; TITLE OF INVENTION: Electronic Medical Record, Library of Electronic Medical Record
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; POLYMORPHISM DATA, AND COMPUTER SYSTEMS AND METHODS FOR USE IN
; FILE REFERENCE: FORS-06443


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; CURRENT APPLICATION NUMBER: US/09/929,135
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-929-135-2

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-929-135-2 (1-14)
QY 38 SerAlaThrSer 41
Db 13 TCTGCCACGCTCA 2

RESULT 278
US-09-837-306-24
; Sequence 24, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-837-306-24

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-837-306-24 (1-14)
QY 169 SerValArgLeu 172
Db 3 TCACTGAGACTC 14

RESULT 279
US-10-325-403-14/c
; Sequence 14, Application US/10325403
; Publication No. US20040033568A9
```

```
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TREATMENT OF DISEASES CAUSED
; BY EXPRESSION OF THE c-MYC
; GENE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION NUMBER: US/10/325,403
; FILING DATE: 23-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/07/936,422
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/241
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-325-403-14

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-325-403-14 (1-14)
QY 104 LeuSerLeuArg 107
Db 12 CTGCTTTTGGCG 1

RESULT 280
US-10-133-642-4
; Sequence 4, Application US/10133642
; Publication No. US20030077693A1
; GENERAL INFORMATION:
; APPLICANT: Jefferies, Wilfred A.
; APPLICANT: McGeer, Patrick L.
; APPLICANT: Rothenberger, Sylvia
; APPLICANT: Food, Michael R.
; APPLICANT: Yamada, Tatsuo
; APPLICANT: Kennard, Malcolm
; TITLE OF INVENTION: Use of p97 and Iron Binding Proteins as Diagnostic and Therapeu
; FILE REFERENCE: 7685-48
```

; CURRENT APPLICATION NUMBER: US/10/133,642
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/285,040
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: US 08/520,933
; PRIOR FILING DATE: 1995-08-31
; PRIOR APPLICATION NUMBER: US 08/367,224
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: PCT/CA93/00272
; PRIOR FILING DATE: 1995-03-30
; PRIOR APPLICATION NUMBER: US 07/912,291
; PRIOR FILING DATE: 1992-07-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-133-642-4

Alignment Scores: 14
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-133-642-4 (1-14)

OY 95 AlaAspPheLeu 98

Db 1 GCGGACTTCCTC 12

RESULT 281

US-10-291-230-45/c
; Sequence 45, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing a
; OTHER INFORMATION: n NruI site.
US-10-291-230-45

Alignment Scores: 14
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0

DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-291-230-45 (1-14)
OY 171 ArgLeuSerArg 174
Db 12 CGGCTCTCGCA 1
RESULT 282
US-10-291-249-45/c
; Sequence 45, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing
; OTHER INFORMATION: n NruI site.
US-10-291-249-45
Alignment Scores: 14
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-291-249-45 (1-14)
OY 171 ArgLeuSerArg 174
Db 12 CGGCTCTCGCA 1
RESULT 283
US-10-325-403-14/c
; Sequence 14, Application US/10325403
; Publication No. US20030162264A1
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TREATMENT OF DISEASES CAUSED
; BY EXPRESSION OF THE c-MYC
; GENE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,403
FILING DATE: 23-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,943
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/936,422
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-325-403-14

Alignment Scores:
Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
DB: 14
Gaps: 0

US-09-966-880A-8 (1-198) x US-10-325-403-14 (1-14)

OY 104 LeuSerLeuArg 107
Db 12 CTGCTTTTGGC 1

RESULT 284

US-10-353-751-2/c
Sequence 2, Application US/10353751
Publication No. US20030219784A1
GENERAL INFORMATION:
APPLICANT: Ip, Hon S.
APPLICANT: Zlatno, Witold A.
APPLICANT: Donald, Glen
TITLE OF INVENTION: Systems and Methods for Analysis of Agricultural Products
FILE REFERENCE: FORS-07809
CURRENT APPLICATION NUMBER: US/10/353,751
CURRENT FILING DATE: 2003-01-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-353-751-2

Alignment Scores:
Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
DB: 15
Gaps: 0

US-09-966-880A-8 (1-198) x US-10-353-751-2 (1-14)
OY 38 SerAlaThrSer 41
Db 13 TCTGCCACGTCA 2

RESULT 285

US-10-045-674-24
Sequence 24, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROONEY, KRISTIN L.
APPLICANT: HOBT, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DVAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-045-674-24

Alignment Scores:
Pred. No.: 14
Score: 3.54e+04
Length: 14
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
DB: 15
Gaps: 0

US-09-966-880A-8 (1-198) x US-10-045-674-24 (1-14)

OY 169 SerValArgLeu 172
Db 3 TCACTGAGACTC 14

RESULT 286

US-10-321-039-754/c
Sequence 754, Application US/10321039
Publication No. US20040014067A1
GENERAL INFORMATION:
APPLICANT: Lyamichiev, Victor
APPLICANT: Lukowiak, Andrew
APPLICANT: Jarvis, Nancy
APPLICANT: Kurensky, David
TITLE OF INVENTION: Amplification Methods and Compositions
FILE REFERENCE: FORS-06960
CURRENT APPLICATION NUMBER: US/10/321,039
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/998,157
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 754
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-039-754

Alignment Scores:
Pred. No.: 3.54e+04 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 15 Gaps: 0

US-09-966-880A-8 (1-198) x US-10-321-039-754 (1-14)

QY 38 SerAlaThrSer 41
DB 13 TCTGCCACGTCA 2

RESULT 287

US-09-767-395-35
; Sequence 35, Application US/09767395
; Patent No. US2002004215A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; Derbyshire, Elaine J
; McCafferty, John G
; Vaughan, Tristan J
; Johnson, Kevin S

TITLE OF INVENTION: Labelling and selection of molecules
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/767,395
FILING DATE: 23-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/098,244
FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
APPLICATION NUMBER: GB 9614292.2
FILING DATE: 08-JUL-1996
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
APPLICATION NUMBER: GB 9712818.5
FILING DATE: 18-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34800

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-767-395-35

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-767-395-35 (1-15)

QY 83 SerTrpSerPro 86
DB 4 TCCTGGAGCCG 15

RESULT 288

US-09-504-231A-82
; Sequence 82, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; Applicant: McSwiggen, James
; Applicant: Roberts, Beth
; Applicant: Pavco, Pamela
; Applicant: Macejak, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA
FILE REFERENCE: Ipi 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: Patentin version 3.0
SEQ ID NO 82
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:

US-09-504-231A-82
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-82 (1-15)

QY 59 LeuLeuPheLeu 62
DB 3 UUGCUUUUCUC 14

RESULT 289

US-09-504-231A-197
; Sequence 197, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; Applicant: McSwiggen, James
; Applicant: Roberts, Beth
; Applicant: Pavco, Pamela

```

; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 197
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-197

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-197 (1-15)

QY 164 GlyLeuHisGlu 167
DB 3 GGCCUUCAGAA 14

RESULT 290
US-09-504-231A-198
; Sequence 198, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-198

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-198 (1-15)

QY 164 GlyLeuHisGlu 167
DB 2 GGCCUUCAGAA 13

RESULT 291
US-09-504-231A-246/c
; Sequence 246, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-246

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-246 (1-15)

QY 72 ProGlyArgCys 75
DB 15 CCCGGAAGATGC 4

RESULT 292
US-09-504-231A-247/c
; Sequence 247, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 199
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-199

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
```

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Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-198 (1-15)

QY 164 GlyLeuHisGlu 167
DB 2 GGCCUUCAGAA 13

RESULT 291
US-09-504-231A-246/c
; Sequence 246, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-246

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-246 (1-15)

QY 72 ProGlyArgCys 75
DB 15 CCCGGAAGATGC 4

RESULT 292
US-09-504-231A-247/c
; Sequence 247, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: fpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 199
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-199

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
```

; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-247

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-247 (1-15)

QY 72 ProGlyArgCys 75
|||
DB 13 CCCGGAAGATGC 2

RESULT 293

US-09-504-231A-248/c
; Sequence 248, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Favco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 248
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-248

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-248 (1-15)

QY 72 ProGlyArgCys 75
|||
DB 12 CCCGGAAGATGC 1

RESULT 294

US-09-504-231A-249
; Sequence 249, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Favco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-249

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-249 (1-15)

QY 125 GlyLeuArgArg 128
|||
DB 4 GGGUUGCGAAGG 15

RESULT 295

US-09-504-231A-321/c
; Sequence 321, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Favco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: rpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24

;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3242
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 321
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-321

Alignment Scores: Length: 15
Pred. No.: 3.78e+04
Score: 4.00
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-321 (1-15)

Qy 123 ProGluGlyLeu 126
Db 12 CCGAGAGGCCTC 1

RESULT 296

US-09-504-231A-369
;; Sequence 369, Application US/09504231A
;; Patent No. US20020013458A1
;; GENERAL INFORMATION:
;; APPLICANT: Blatt, Lawrence
;; APPLICANT: McSwiggen, James
;; APPLICANT: Roberts, Beth
;; APPLICANT: Pavco, Pamela
;; APPLICANT: Macejak, Dennis
;; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

;; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
;; FILE REFERENCE: tpi 247/282
;; CURRENT APPLICATION NUMBER: US/09/504,231A
;; CURRENT FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: 09/274,553
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 09/257,608
;; PRIOR FILING DATE: 1999-02-24
;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3242
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 369
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-369

Alignment Scores: Length: 15
Pred. No.: 3.78e+04
Score: 4.00
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-369 (1-15)

Qy 128 ArgLeuHisArg 131
Db 12 CCGAGAGGCCTC 1

Db 4 CGGUUGCACAGG 15
RESULT 297
US-09-504-231A-481
;; Sequence 481, Application US/09504231A
;; Patent No. US20020013458A1
;; GENERAL INFORMATION:
;; APPLICANT: Blatt, Lawrence
;; APPLICANT: McSwiggen, James
;; APPLICANT: Roberts, Beth
;; APPLICANT: Pavco, Pamela
;; APPLICANT: Macejak, Dennis
;; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

;; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
;; FILE REFERENCE: tpi 247/282
;; CURRENT APPLICATION NUMBER: US/09/504,231A
;; CURRENT FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: 09/274,553
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 09/257,608
;; PRIOR FILING DATE: 1999-02-24
;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3242
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 481
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-481

Alignment Scores: Length: 15
Pred. No.: 3.78e+04
Score: 4.00
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-481 (1-15)

Qy 2 AspSerLeuLeu 5
Db 4 GACUCACUCUU 15

RESULT 298

US-09-504-231A-549
;; Sequence 549, Application US/09504231A
;; Patent No. US20020013458A1
;; GENERAL INFORMATION:
;; APPLICANT: Blatt, Lawrence
;; APPLICANT: McSwiggen, James
;; APPLICANT: Roberts, Beth
;; APPLICANT: Pavco, Pamela
;; APPLICANT: Macejak, Dennis
;; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT

;; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
;; FILE REFERENCE: tpi 247/282
;; CURRENT APPLICATION NUMBER: US/09/504,231A
;; CURRENT FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: 09/274,553
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 09/257,608
;; PRIOR FILING DATE: 1999-02-24
;; PRIOR APPLICATION NUMBER: 60/100,842
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/083,217
;; PRIOR FILING DATE: 1998-04-27
;; NUMBER OF SEQ ID NOS: 3242
;; DB: 0

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 549
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-549

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-549 (1-15)

Qy 59 LeuLeuPheLeu 62
|||||
Db 1 UUGCUUUCUC 12

RESULT 299

US-09-504-231A-711
; Sequence 711, Application US/09504231A

; Patent No. US20020013458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: Macejak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: IPI 247/282

; CURRENT APPLICATION NUMBER: US/09/504,231A

; PRIOR FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: 09/274,553

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3242

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 711

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-504-231A-711

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-711 (1-15)

Qy 59 LeuLeuPheLeu 62
|||||
Db 3 UUGCUUUCUCU 14

RESULT 300

US-09-504-231A-712

; Sequence 712, Application US/09504231A

; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-712

Alignment Scores:
Pred. No.: 3.78e+04 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-504-231A-712 (1-15)

Qy 59 LeuLeuPheLeu 62
|||||
Db 2 UUGCUUUCUCU 13

Search completed: March 5, 2004, 03:19:31
Job time : 358 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 5, 2004, 00:23:04 ; Search time 80 Seconds
(without alignments)
1373.503 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198
Sequence: 1 MDSLLMNRKFLYQKXVRW.....ILLPLYEVDLRLDAFRTGL 198

Scoring table:
OLIGO Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 348605

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US0966880/runat_04032004_083153_22415/app_query.fasta_1.391
-DB=issued Patents NA -QWMT=fastap -SUFFIX=Oligo.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -WAXLEN=20
-USER=US0966880 @CGN_1.1.69 @runat_04032004_083153_22415 -NCPU=6 -ICPU=3
-NO WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	3.0	18	US-09-422-978-11764	Sequence 11764, A
2	6	3.0	19	US-09-422-978-7618	Sequence 7618, Ap
3	6	3.0	20	US-08-651-692-2	Sequence 2, Appli
4	6	3.0	20	US-09-907-843-27	Sequence 27, Appl
5	6	3.0	20	US-09-422-978-9310	Sequence 9310, Ap
6	6	3.0	20	US-09-198-452A-5376	Sequence 5376, Ap
7	5	2.5	15	US-09-081-646-727	Sequence 727, App
8	5	2.5	16	US-07-664-989B-101	Sequence 101, App
9	5	2.5	16	PCT-US94-06331A-20	Sequence 20, Appl
10	5	2.5	17	US-08-758-306-583	Sequence 583, App
11	5	2.5	17	US-08-758-306-585	Sequence 585, App
12	5	2.5	17	US-08-292-620A-1635	Sequence 1635, Ap

13	5	2.5	17	US-08-292-620A-1631	Sequence 1691, Ap
14	5	2.5	17	US-08-292-620A-1891	Sequence 1891, Ap
15	5	2.5	17	US-08-292-620A-1581	Sequence 1891, Ap
16	5	2.5	17	US-08-292-620A-1586	Sequence 1886, Ap
17	5	2.5	17	US-09-071-845-1635	Sequence 1635, Ap
18	5	2.5	17	US-09-071-845-1691	Sequence 1691, Ap
19	5	2.5	17	US-09-071-845-1891	Sequence 1891, Ap
20	5	2.5	17	US-09-071-845-1891	Sequence 1891, Ap
21	5	2.5	17	US-09-071-845-1896	Sequence 1886, Ap
22	5	2.5	17	US-08-584-040-2010	Sequence 2010, Ap
23	5	2.5	17	US-08-584-040-2011	Sequence 2011, Ap
24	5	2.5	17	US-08-584-040-4354	Sequence 4354, Ap
25	5	2.5	17	US-08-584-040-4355	Sequence 4355, Ap
26	5	2.5	17	US-08-584-040-4356	Sequence 4356, Ap
27	5	2.5	17	US-08-584-040-7303	Sequence 7303, Ap
28	5	2.5	17	US-08-584-040-7304	Sequence 7304, Ap
29	5	2.5	17	US-08-676-342A-31	Sequence 31, Appl
30	5	2.5	17	US-09-474-432B-346	Sequence 346, App
31	5	2.5	17	US-09-371-772B-555	Sequence 555, App
32	5	2.5	17	US-09-371-772B-556	Sequence 556, App
33	5	2.5	17	US-09-371-772B-2121	Sequence 2121, Ap
34	5	2.5	17	US-09-371-772B-2122	Sequence 2122, Ap
35	5	2.5	17	US-09-371-772B-2123	Sequence 2123, Ap
36	5	2.5	17	US-09-371-772B-3112	Sequence 3112, Ap
37	5	2.5	17	US-09-371-772B-3113	Sequence 3113, Ap
38	5	2.5	17	US-09-371-772B-4848	Sequence 4848, Ap
39	5	2.5	17	US-09-476-387-345	Sequence 345, App
40	5	2.5	17	US-09-866-108A-9581	Sequence 9581, Ap
41	5	2.5	17	US-09-866-108A-9582	Sequence 9582, Ap
42	5	2.5	17	US-09-866-108A-9583	Sequence 9583, Ap
43	5	2.5	17	US-09-866-108A-9630	Sequence 9630, Ap
44	5	2.5	17	US-09-866-108A-9631	Sequence 9631, Ap
45	5	2.5	17	US-09-866-108A-9632	Sequence 9632, Ap

ALIGNMENTS

RESULT 1
US-09-422-978-11764
; Sequence 11764, Application US/09422378
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422, 978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298, 850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109, 732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082, 614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in complemen
US-09-422-978-11764

Alignment Scores:
Pred. No.: 87.3 Length: 18
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-422-978-11764 (1-18)

Qy 179 ILeuLeuProLeuTyr 184
Db 1 ATCCTTCTCCCACTCTAC 18

RESULT 2

US-09-422-978-7618/c
; Sequence 7618, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7618
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-9709 for SEQ 3684,
US-09-422-978-7618

Alignment Scores:

Pred. No.:	92	Length:	19
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-422-978-7618 (1-19)

Qy 167 GluAsnSerValArgLeu 172
Db 19 GAAATAGTGTAGGCTC 2

RESULT 3

US-09-651-692-2
; Sequence 2, Application US/08651692
; Patent No. 5856099
; GENERAL INFORMATION:
; APPLICANT: Loren Miraglia, Thomas Geiger
; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,692
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-651-692-2

Alignment Scores:	96.8	Length:	20
Pred. No.:	6.00	Matches:	6
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x US-08-651-692-2 (1-20)

Qy 125 GlyLeuArgArgLeuHis 130
Db 2 GGGCTGCGCGCTCCAC 19

RESULT 4

US-09-907-843-27/c
; Sequence 27, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-27

Alignment Scores:	96.8	Length:	20
Pred. No.:	6.00	Matches:	6
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-907-843-27 (1-20)

Qy 122 GluProGlyLeuArg 127
Db 18 GAGCCTGAGGCGCTCGCG 1

RESULT 5

US-09-422-978-9310

```

; Sequence 9310, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENST.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9310
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20_bind
; OTHER INFORMATION: downstream amplification primer 99-24508 for SEQ 1445, in complement
US-09-422-978-9310

Alignment Scores:
Pred. No.: 96.8 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-9310 (1-20)

QY 40 ThrSerPheSerLeuAsp 45
Db 2 ACAAGTTTCATTAGAC 19

RESULT 6
US-09-198-452A-5376
; Sequence 5376, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5376
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5376

Alignment Scores:
Pred. No.: 96.8 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.03% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-5376 (1-20)

QY 167 GluAsnSerValArgLeu 172
Db 1 GAGACTCGGTGGCGCTG 18

```

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RESULT 7
US-09-081-646-727
; Sequence 727, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and Cancer Cells
; FILE REFERENCE: 01107.74864
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 727
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-727

Alignment Scores:
Pred. No.: 839 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-081-646-727 (1-15)

QY 93 HisValAlaAspPhe 97
Db 1 CATGTGCTGACTTT 15

RESULT 8
US-07-664-989B-101
; Sequence 101, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/487,063
;; FILING DATE: 02-MAR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/240,160
;; FILING DATE: 02-SEP-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cooper, Iver P.
;; REGISTRATION NUMBER: 28005
;; REFERENCE/DOCKET NUMBER: LADNER 7
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: genomic DNA
US-07-664-989B-101

Alignment Scores:
Pred. No.: 894 Length: 16
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-664-989B-101 (1-16)

QY 178 ArcileuleuPro 182
DB 1 CGGATCCTCCTCCCT 15

RESULT 9
PCT-US94-06331A-20/c
; Sequence 20, Application PC/TUS9406331A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF FIBROSIS AND
; TITLE OF INVENTION: FIBROUS TISSUE DISEASE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06331A
; FILING DATE: June 2, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

none

;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US94-06331A-20

Alignment Scores:
Pred. No.: 894 Length: 16
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-06331A-20 (1-16)

QY 21 Alalyesglyvarg 25
DB 15 GCAGAGGTAGGAGG 1

RESULT 10
US-08-758-306-583/c
; Sequence 583, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-583

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-758-306-583 (1-17)

QY 124 GluglyLeuArg 128
Db 17 GAAGGACTAAGAAGG 3

RESULT 11
US-08-758-306-585/c
; Sequence 585, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 585:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-758-306-585
Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-758-306-585 (1-17)

QY 124 GluglyLeuArg 128
Db 16 GAAGGACTAAGAAGG 2

RESULT 12
US-08-292-620A-1635
; Sequence 1635, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1635:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-292-620A-1635
Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1635 (1-17)

QY 58 GluLeuPheLeu 62

Db 1 GAACUGCUCUCCUC 15

RESULT 13
US-08-292-620A-1691
; Sequence 1691, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1691:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1691

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1691 (1-17)

Qy 58 GluLeuLeuPheLeu 62

Db 1 GAACUGCUCUCCUC 15

RESULT 15

RESULT 14

US-08-292-620A-1891
; Sequence 1891, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1891:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1891

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1891 (1-17)

Qy 58 GluLeuLeuPheLeu 62

Db 1 GAACUGCUCUCCUC 15

two

two

US-08-292-620A-1981
; Sequence 1981, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1981

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1981 (1-17)
QY 58 GluLeuLeuPheLeu 62
Db 1 GAACUGCUCUCCUC 15
RESULT 16
US-08-292-620A-1986
; Sequence 1986, Application US/08292620A

Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1986:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-292-620A-1986

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-292-620A-1986 (1-17)
QY 58 GluLeuLeuPheLeu 62
Db 1 GAACUGCUCUCCUC 15
RESULT 17
US-09-071-845-1635
; Sequence 1635, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:

two

two

APPLICANT: Susan Grimm
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James McSwiggen
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth G. Draper
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: INTRACELLULAR ADHESION
 TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
 NUMBER OF SEQUENCES: 2390
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,845
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/292,620
 FILING DATE: August 17, 1994
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/149
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1635:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-071-845-1635

Alignment Scores: 949 Length: 17
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 3

US-09-966-880A-8 (1-198) x US-09-071-845-1635 (1-17)

QY 58 GluleuLeuPheLeu 62
 Db 1 GAACUGCUCUCCUC 15

RESULT 18

US-09-071-845-1691
 ; Sequence 1691, Application US/09071845
 ; Patent No. 6132967
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm
 ; APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen
 APPLICANT: Sean Sullivan
 APPLICANT: Kenneth G. Draper
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 TITLE OF INVENTION: DISEASES OR CONDITIONS
 TITLE OF INVENTION: RELATED TO LEVELS OF
 TITLE OF INVENTION: INTRACELLULAR ADHESION
 TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
 NUMBER OF SEQUENCES: 2390
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,845
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/292,620
 FILING DATE: August 17, 1994
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/149
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 1691:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-071-845-1691

Alignment Scores: 949 Length: 17
 Pred. No.: 5.00 Matches: 5
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 2.53% Gaps: 0
 DB: 3

US-09-966-880A-8 (1-198) x US-09-071-845-1691 (1-17)

QY 58 GluleuLeuPheLeu 62
 Db 1 GAACUGCUCUCCUC 15

RESULT 19

US-09-071-845-1891
 ; Sequence 1891, Application US/09071845
 ; Patent No. 6132967
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggen
 ; APPLICANT: Sean Sullivan


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; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1891:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1891

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1891 (1-17)

QY 58 GluLeuLeuPheLeu 62
Db 1 GAACGUCUCUCCUC 15

RESULT 20
US-09-071-845-1891
; Sequence 1891, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

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; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1981

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1981 (1-17)

QY 58 GluLeuLeuPheLeu 62
Db 1 GAACGUCUCUCCUC 15

RESULT 21
US-09-071-845-1986
; Sequence 1986, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

;; TITLE OF INVENTION: INTRACELLULAR ADHESION
;; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
;; NUMBER OF SEQUENCES: 2390
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/071,845
;; FILING DATE: US/09/071,845
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/292,620
;; FILING DATE: August 17, 1994
;; APPLICATION NUMBER: 08/008,895
;; FILING DATE: January 19, 1993
;; APPLICATION NUMBER: 07/989,849
;; FILING DATE: December 7, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 208/149
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1986:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-071-845-1986

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-071-845-1986 (1-17)

QY 58 GluLeuLeuPheLeu 62
Db 1 GAACUGCUUCCUC 15

RESULT 22

US-08-584-040-2010
; Sequence 2010, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2010:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-584-040-2010

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-2010 (1-17)

QY 102 ProAsnLeuSerLeu 106
Db 3 CCGAUCUUCUUG 17

RESULT 23

US-08-584-040-2011
; Sequence 2011, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

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; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2011:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2011
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; Alignment Scores:
; Pred. No.: 949 Length: 17
; Score: 5.00 Matches: 5
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.53% Indels: 0
; DB: 4 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-584-040-2011 (1-17)
;
; QY 102 ProAsnLeuSerLeu 106
; DB 1 CCGAUAUUAUUCUUG 15
;
; RESULT 24
; US-08-584-040-4354
; Sequence 4354, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4354:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-4354
;
; Alignment Scores:
; Pred. No.: 949 Length: 17
; Score: 5.00 Matches: 5
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.53% Indels: 0
; DB: 4 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-584-040-4354 (1-17)
;
; QY 157 ArgThrPheLysAla 161
; DB 3 AGAACUUUAAGCU 17
;
; RESULT 25
; US-08-584-040-4355
; Sequence 4355, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995

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ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4355:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4355

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-4355 (1-17)
QY 157 ArgThrPheLysAla 161
Db 2 AGAACUUUUAAAGCU 16

RESULT 26
US-08-584-040-4356
Sequence 4356, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4356:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4356

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-4356 (1-17)
QY 157 ArgThrPheLysAla 161
Db 1 AGAACUUUUAAAGCU 15

RESULT 27
US-08-584-040-7303
Sequence 7303, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7303:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

US-08-584-040-7303
Alignment Scores:
Pred. No.: 949
Score: 5.00
Length: 17
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Indels: 0
Query Match: 2.53%
DB: 4
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-7303 (1-17)
QY 179 IleLeuLeuProLeu 183
DB 2 AUACUCUUACCCUG 16

RESULT 28
US-08-584-040-7304
; Sequence 7304, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7304:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7304
Alignment Scores:
Pred. No.: 949
Score: 5.00
Length: 17
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Indels: 0
Query Match: 2.53%
DB: 4
Gaps: 0

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Query Match: 2.53%
DB: 4
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-584-040-7304 (1-17)
QY 179 IleLeuLeuProLeu 183
DB 1 AUACUCUUACCCUG 15

RESULT 29
US-08-676-342A-31/c
; Sequence 31, Application US/08676342A
; Patent No. 6348313
; GENERAL INFORMATION:
; APPLICANT: SIBSON, DAVID R.
; TITLE OF INVENTION: Sequencing of Nucleic Acids
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd. Suite 1400
; CITY: Arlington
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,342A
; FILING DATE: 19-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00109
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401200.2
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: HLBB 4
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleotides
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-676-342A-31
Alignment Scores:
Pred. No.: 949
Score: 5.00
Length: 17
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Indels: 0
Query Match: 2.53%
DB: 4
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-676-342A-31 (1-17)
QY 104 LeuSerLeuArgile 108
DB 15 CTTTCACTCGAATT 1

RESULT 30
US-08-474-432B-346
; Sequence 346, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

```

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Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-555 (1-17)

Qy 102 ProAsnLeuSerLeu 106
Db 3 CCGAAUCUACUUG 17

RESULT 32
US-09-371-772B-556
; Sequence 556, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 556
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-556

Alignment Scores: 17
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-555 (1-17)

Qy 102 ProAsnLeuSerLeu 106
Db 1 CCGAAUCUACUUG 15

RESULT 33
US-09-371-772B-2121
; Sequence 2121, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2121
; LENGTH: 17

```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2121

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-2121 (1-17)

QY 157 ArgThrPheLysAla 161
Db 3 AGAACUUUAAGCU 17

RESULT 34

US-09-371-772B-2122
; Sequence 2122, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2122

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-2122 (1-17)

QY 157 ArgThrPheLysAla 161
Db 2 AGAACUUUAAGCU 16

RESULT 35

US-09-371-772B-2123
; Sequence 2123, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2123
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2123

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-2123 (1-17)

QY 157 ArgThrPheLysAla 161
Db 1 AGAACUUUAAGCU 15

RESULT 36

US-09-371-772B-3112
; Sequence 3112, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3112
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3112

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-3112 (1-17)

QY 179 IleuleuProLeu 183
Db 2 AUACUCUUAACCCUG 16

RESULT 37

US-09-371-772B-3113
; Sequence 3113, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3113
LENGTH: 17
TYPE: RNA
ORGANISM: Mus sp.
US-09-371-772B-3113

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-3113 (1-17)

QY 179 ileLeuLeuProLeu 183
Db 1 AUAUCUUAUCCUUG 15

RESULT 38
US-09-371-772B-4848
Sequence 4848, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4848
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-4848

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-371-772B-4848 (1-17)

QY 102 ProAenLeuSerLeu 106
Db 2 CCGAUAUCUUAUUG 16
RESULT 39
US-09-476-387-345
Sequence 345, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MBH00-831-C (243/073)
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/083,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/064,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 345
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-476-387-345

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-476-387-345 (1-17)

QY 89 AspCysAlaArgHis 93
Db 3 GAUUGUGCGAGGCAC 17

RESULT 40
US-09-866-108A-9581/c
Sequence 9581, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: Ji, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359


```

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9581
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9581

Alignment Scores:
Pred. No.: 949          Length: 17
Score: 5.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9581 (1-17)

QY 41 SerPheSerLeuAsp 45
DB 17 AGCTTTTCCTCGAC 3

RESULT 41
US-09-866-108A-9582/c
; Sequence 9582, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9583
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9583

Alignment Scores:

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9582
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9582

Alignment Scores:
Pred. No.: 949          Length: 17
Score: 5.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9582 (1-17)

QY 41 SerPheSerLeuAsp 45
DB 16 AGCTTTTCCTCGAC 2

RESULT 42
US-09-866-108A-9583/c
; Sequence 9583, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9583
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9583

Alignment Scores:

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Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9583 (1-17)

Qy 41 SerPheSerLeuasp 45
|||||
Db 15 AGCTTTTCCCGAC 1

RESULT 43

US-09-866-108A-9630
; Sequence 9630, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 9630

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-9630

Alignment Scores:
Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9630 (1-17)

Qy 124 GluclyleuArgarg 128
|||||
Db 3 GAAGGGCTCCGAGG 17

RESULT 44

US-09-866-108A-9631
; Sequence 9631, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aeomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 9631

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-9631

Alignment Scores:

Pred. No.: 949 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9631 (1-17)

Qy 124 GluclyleuArgarg 128
|||||
Db 2 GAAGGGCTCCGAGG 16

RESULT 45

US-09-866-108A-9632
; Sequence 9632, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

```

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9632
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9632

Alignment Scores:
Pred. No.: 949      Length: 17
Score: 5.00        Matches: 5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4              Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9632 (1-17)

QY 124 GluGlyLeuArgArg 128
Db 1 GAAGGGCTCCGAGG 15

RESULT 46
US-09-866-108A-9765
; Sequence 9765, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9765
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9765

Alignment Scores:
Pred. No.: 949      Length: 17
Score: 5.00        Matches: 5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4              Gaps: 0

US-09-966-880A-8 (1-198) x US-09-866-108A-9765 (1-17)

QY 103 AsnLeuSerLeuArg 107
Db 3 AACCTCTCGTGAGG 17

RESULT 47
US-09-866-108A-9766
; Sequence 9766, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

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Patent No. 6686188
SEQ ID NO 9766
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-9766

Alignment Scores:
Pred. No.: 949
Score: 5.00
Length: 17
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-09-866-108A-9766 (1-17)

QY 103 AsnLeuSerLeuArg 107
DB 2 AACCTCTCGCTGAGG 16

RESULT 49
US-09-866-108A-9767
Sequence 9767, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: A600100000-10-04
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: A600100000 Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 9767
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-9767

Alignment Scores:
Pred. No.: 949
Score: 5.00
Length: 17
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0

DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-866-108A-9767 (1-17)
QY 103 AsnLeuSerLeuArg 107
DB 1 AACCTCTCGCTGAGG 15

RESULT 49
US-07-977-284A-44
Sequence 44, Application US/07977284A
Patent No. 5558988
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofar Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589888ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,284A
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
US-07-977-284A-44

Alignment Scores:
Pred. No.: 1e+03
Score: 5.00
Length: 18
Matches: 5
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.53%
Indels: 0
Gaps: 0
DB:

US-09-966-880A-8 (1-198) x US-07-977-284A-44 (1-18)

QY 69 AsnLeuSerLeuArg 173
DB 3 GATCTGGATCTGGA 17

RESULT 50

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US-08-390-850-1123/c
; Sequence 1123, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; FILING DATE: December 13, 1994
; FILING DATE: No. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600.
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-390-850-1123
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-390-850-1123 (1-18)
Qy 119 ArgLyseAlaGluPro 123
Db 15 AGAAGCGGGAACCG 1
RESULT 51
US-08-435-634-1123/c
; Sequence 1123, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela

```

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; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-1123
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-435-634-1123 (1-18)
Qy 119 ArgLyseAlaGluPro 123
Db 15 AGAAGCGGGAACCG 1
RESULT 52
US-08-453-956-2
; Sequence 2, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY

```

STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,956
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,631
FILING DATE: July 1, 1993
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC976
US-08-453-956-2

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-453-956-2 (1-18)

QY 32 ValVallyeArgArg 36
DB 2 GTGTAAACGACGG 16

RESULT 53
US-08-086-631-2
Sequence 2, Application US/08086631
Patent No. 5776725
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
TITLE OF INVENTION: GLUCAGON RECEPTORS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COLUMBIA CENTER
CITY: SEATTLE
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ZC976
US-08-086-631-2

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-086-631-2 (1-18)

QY 32 ValVallyeArgArg 36
DB 2 GTGTAAACGACGG 16

RESULT 54
US-08-468-551-3
Sequence 3, Application US/08468551
Patent No. 5874212
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Rock, Matthew J.
APPLICANT: Garguly, Arupa
TITLE OF INVENTION: DETECTION OF SINGLE BASE MUTATIONS AND
TITLE OF INVENTION: OTHER VARIATIONS IN DOUBLE STRANDED DNA BY
TITLE OF INVENTION: CONFORMATION-SENSITIVE CELL ELECTROPHORESIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: UNITED STATES
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,551
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Doyle Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9855-5U1
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 3:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-551-3

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-468-551-3 (1-18)

QY 69 AspLeuAspProgly 73
Db 3 GATCTGGATCTTGGG 17

RESULT 55
US-08-532-727A-18/c
; Sequence 18, Application US/08532727A
; Patent No. 5833239
; GENERAL INFORMATION:
; APPLICANT: ANDRIEN, MARC
; APPLICANT: DUPONT, ETIENNE
; APPLICANT: ROSSAU, RUDI
; APPLICANT: DECKANCK ILSE
; TITLE OF INVENTION: PROCESS FOR TYPING HLA-B USING SPECIFIC PRIMERS
; TITLE OF INVENTION: AND PROBES SETS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,727A
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-9
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Oligonucleotide Probe 12
; LOCATION: anneals to nucleotides 189-206 of exon 2 of HLA-
US-08-532-727A-18

Alignment Scores:
Pred. No.: 1e+03 Length: 18

```

```

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-532-727A-18 (1-18)

QY 112 ArgLeuTy-PheCys 116
Db 17 CGCTTGACTTCTGT 3

RESULT 56
US-08-452-930-2
; Sequence 2, Application US/08452930
; Patent No. 5919635
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,930
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; CLONE: ZC976
US-08-452-930-2

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-452-930-2 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 57

```

US-08-256-426B-44
; Sequence 44, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; CORRESPONDENCE ADDRESSES: 293
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-256-426B-44
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x US-08-256-426B-44 (1-18)
QY 69 AspleuaspProgly 73
Db 3 GAICTGATCTCTAGA 17
RESULT 58
US-09-213-767-47/c
; Sequence 47, Application US/09213767
; Patent No. 5948680
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION

; FILE REFERENCE: RTS-0024
; CURRENT APPLICATION NUMBER: US/09/213,767
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-213-767-47
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x US-09-213-767-47 (1-18)
QY 103 AsnLeuSerLeuArg 107
Db 17 AACCTTCTCTCAGA 3
RESULT 59
US-09-205-144-10
; Sequence 10, Application US/09205144
; Patent No. 5958771
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESSION
; FILE REFERENCE: RTS-0021
; CURRENT APPLICATION NUMBER: US/09/205,144
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-144-10
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: Gaps: 0
US-09-966-880A-8 (1-198) x US-09-205-144-10 (1-18)
QY 59 LeuLeuPheLeuArg 63
Db 4 CTATTATCTCTAGA 18
RESULT 60
US-09-205-144-42
; Sequence 42, Application US/09205144
; Patent No. 5958771
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESSION
; FILE REFERENCE: RTS-0021
; CURRENT APPLICATION NUMBER: US/09/205,144
; CURRENT FILING DATE: 1998-12-03


```
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-144-42

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 2                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-205-144-42 (1-18)
QY 38 SerAlaThrSerPhe 42
Db 4 AGTGCTACCTCTTT 18

RESULT 61
US-09-211-631-19
; Sequence 19, Application US/09211631
; Patent No. 6001597
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; APPLICANT: Vanaja, Erica
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDES IN FICHA METHANOLICA
; FILE REFERENCE: 96-16C2
; CURRENT APPLICATION NUMBER: US/09/211,631
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-09-211-631-19

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-211-631-19 (1-18)
QY 32 ValValIysArgArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 62
US-09-205-921-13
; Sequence 13, Application US/09205921A
; Patent No. 6003048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 18
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-921-13

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-205-921-13 (1-18)
QY 127 ArgArgLeuHisArg 131
Db 4 CGCGCGCTCCACGC 18

RESULT 63
US-09-357-072-30/c
; Sequence 30, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-30

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatives: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-357-072-30 (1-18)
QY 43 SerLeuAspPheGly 47
Db 17 AGCCTGGACTTGGT 3

RESULT 64
US-09-081-180-17
; Sequence 17, Application US/09081180
; Patent No. 6022847
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT:
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC976
; US-09-081-180-17
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-081-180-17 (1-18)
;
; QY 32 ValVallysAATGATG 36
; DB 2 GTTGTAACACGCG 16
;
; RESULT 65
; US-09-040-786-17
; Sequence 17, Application US/09040786
; Patent No. 6025197
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG32
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave. E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,786
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,263
```

```
; FILING DATE: March 19, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan E
; REGISTRATION NUMBER: 41,156
; REFERENCE/DOCKET NUMBER: 97-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC976
; US-09-040-786-17
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-040-786-17 (1-18)
;
; QY 32 ValVallysAATGATG 36
; DB 2 GTTGTAACACGCG 16
;
; RESULT 66
; US-09-143-212-52/c
; Sequence 52, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Moria and Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-143-212-52
;
; Alignment Scores:
; Pred. No.: 1e+03
; Score: 5.00
; Percent Similarity: 100.00%
; Best Local Similarity: 100.00%
; Query Match: 2.53%
; DB: 3
; Length: 18
; Matches: 5
; Conservative: 0
; Mismatches: 0
; Indels: 0
; Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-09-143-212-52 (1-18)
;
; QY 121 AlaGluProGluGly 125
; DB 16 GCTGAGCCTGAAGGA 2
;
; RESULT 67
; US-09-265-628-19
; Sequence 19, Application US/09265628
; Patent No. 6153424
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
```

```
/ APPLICANT: Vanaja, Erica
/ TITLE OF INVENTION: PROTEASE-DEFICIENT STRAINS OF PICHIA
/ TITLE OF INVENTION: METHANOLICA
/ FILE REFERENCE: 97-01C1
/ CURRENT APPLICATION NUMBER: US/09/265,628
/ CURRENT FILING DATE: 1999-03-09
/ EARLIER APPLICATION NUMBER: US 09/152,180
/ EARLIER FILING DATE: 1998-09-11
/ EARLIER APPLICATION NUMBER: US 60/058,822
/ EARLIER FILING DATE: 1997-09-15
/ EARLIER APPLICATION NUMBER: US 08/703,807
/ EARLIER FILING DATE: 1996-08-26
/ EARLIER APPLICATION NUMBER: US 60/042,910
/ EARLIER FILING DATE: 1996-07-17
/ EARLIER APPLICATION NUMBER: US 60/006,397
/ EARLIER FILING DATE: 1995-11-09
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide primer
US-09-265-628-19

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-265-628-19 (1-18)

QY 32 ValValVyeaGcArg 36
Db 2 GTGTAAACACGCG 16

RESULT 68
US-08-413-740A-172
/ Sequence 172, Application US/08413740A
/ Patent No. 6171859
/ GENERAL INFORMATION:
/ APPLICANT: HERRNSTADT, CORINNA
/ APPLICANT: PARKER, WILLIAM D.
/ APPLICANT: DAVIS, ROBERT
/ APPLICANT: MILLER, SCOTT W.
/ TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
/ TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
/ TITLE OF INVENTION: Defects
/ NUMBER OF SEQUENCES: 206
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kenyon & Kenyon
/ STREET: 1025 Connecticut Avenue, N.W.
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20036-5405
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/413,740A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04063
/ FILING DATE: 30-MAR-1995
/ APPLICATION NUMBER: 08/413,740
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/ FILING DATE: 30-MAR-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Botham, David B.
/ REGISTRATION NUMBER: 34297
/ REFERENCE/DOCKET NUMBER: 2105/7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 429-1776
/ TELEFAX: (202) 429-0796
/ INFORMATION FOR SEQ ID NO: 172:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-08-413-740A-172

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-413-740A-172 (1-18)

QY 125 GlyIeuargArgLeu 129
Db 2 GGTCTACGGAGGCTC 16

RESULT 69
US-09-001-141-17
/ Sequence 17, Application US/09001141
/ Patent No. 6183953
/ GENERAL INFORMATION:
/ APPLICANT: Raymond, Christopher K.
/ TITLE OF INVENTION: CHROMOSOMAL MUTAGENESIS IN
/ TITLE OF INVENTION: PICHIA METHANOLICA
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/001,141
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/058,822
/ FILING DATE: 15-SEP-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, Gary E
/ REGISTRATION NUMBER: 31,648
/ REFERENCE/DOCKET NUMBER: 97-70
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6673
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ZC976
US-09-001-141-17

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-001-141-17 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAACGACGG 16

RESULT 70
US-09-140-804-12
; Sequence 12, Application US/09140804
; Patent No. 6137930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-140-804-12

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-140-804-12 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAACGACGG 16

RESULT 71
US-09-630-706-70/c
; Sequence 70, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Coweert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-70

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 3                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-630-706-70 (1-18)
Qy 186 ValAspAspLeuArg 190
Db 17 GTTGATGACCTTCGG 3

RESULT 72
US-09-522-217-77
; Sequence 77, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-522-217-77

Alignment Scores:
Pred. No.: 1e+03      Length: 18
Score: 5.00          Matches: 5
Percent Similarity: 100.00%  Conservatative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.53%      Indels: 0
DB: 4                Gaps: 0

US-09-966-880A-8 (1-198) x US-09-522-217-77 (1-18)
Qy 32 ValVallyysArg 36
Db 2 GTTGTAACGACGG 16

RESULT 73
US-09-653-403-20
; Sequence 20, Application US/09653403
; Patent No. 6348331
; GENERAL INFORMATION:

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; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 2
; TITLE OF INVENTION: PROMOTER AND TERMINATOR
; FILE REFERENCE: 98-57
; CURRENT APPLICATION NUMBER: US/09/653,403
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-653-403-20

Alignment Scores:
Pred. No.:      1e+03      Length:      18
Score:          5.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             4         Gaps:        0

US-09-966-880A-8 (1-198) x US-09-653-403-20 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 74
US-09-294-531B-10
; Sequence 10, Application US/09294531B
; Patent No. 6372889
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Farrah, Theresa M.
; APPLICANT: Mauer, Mark F.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: SOLUBLE PROTEIN ZTMP0-1
; FILE REFERENCE: 97-67
; CURRENT APPLICATION NUMBER: US/09/294,531B
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 60/082,513
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-294-531B-10

Alignment Scores:
Pred. No.:      1e+03      Length:      18
Score:          5.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             4         Gaps:        0

US-09-966-880A-8 (1-198) x US-09-294-531B-10 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 75
US-09-434-408-12
; Sequence 12, Application US/09434408

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; Patent No. 6440697
; GENERAL INFORMATION:
; APPLICANT: Venezia, Domenick
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
; FILE REFERENCE: 98-41
; CURRENT APPLICATION NUMBER: US/09/434,408
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 60/108,258
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-434-408-12

Alignment Scores:
Pred. No.:      1e+03      Length:      18
Score:          5.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             4         Gaps:        0

US-09-966-880A-8 (1-198) x US-09-434-408-12 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 76
US-10-013-784-20
; Sequence 20, Application US/10013784
; Patent No. 6440720
; GENERAL INFORMATION:
; APPLICANT: Raymond, Christopher K.
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE
; TITLE OF INVENTION: DEHYDROGENASE 2
; TITLE OF INVENTION: PROMOTER AND TERMINATOR
; FILE REFERENCE: 98-57
; CURRENT APPLICATION NUMBER: US/10/013,784
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/09/653,403
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-013-784-20

Alignment Scores:
Pred. No.:      1e+03      Length:      18
Score:          5.00      Matches:      5
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.53%      Indels:      0
DB:             4         Gaps:        0

US-09-966-880A-8 (1-198) x US-10-013-784-20 (1-18)

QY      32 ValVallysArgArg 36
Db      2 GTTGTAAACGACGG 16

RESULT 77

```

```
US-08-171-384A-7/C
; Sequence 7, Application US/08171384A
; Patent No. 6475781
; GENERAL INFORMATION:
; APPLICANT: Mercola, Mark K.
; APPLICANT: Deisinger, Prescott L.
; APPLICANT: Stiles, Charles D.
; TITLE OF INVENTION: TRANS-DOMINANT SUPPRESSOR GENES FOR
; TITLE OF INVENTION: OLIGOMERIC PROTEINS
; FILE REFERENCE: 00530-075001
; CURRENT APPLICATION NUMBER: US/08/171.384A
; CURRENT FILING DATE: 1993-12-21
; PRIOR APPLICATION NUMBER: 07/846,972
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: 07/525,245
; PRIOR FILING DATE: 1990-05-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-171-384A-7
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-171-384A-7 (1-18)
QY 59 LeuLeuphelaArg 63
Db 17 CTCTCTCTCTGCGA 3
RESULT 78
US-09-153-242-8/C
; Sequence 8, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundeborg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pUC18/pRIT28,
; OTHER INFORMATION: forward, modulating module, generic
US-09-153-242-8
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-153-242-8 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 3
RESULT 79
US-09-686-838B-12
; Sequence 12, Application US/09686838B
; Patent No. 6482612
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: Adipocyte-Specific Protein Homologs
; FILE REFERENCE: 97-49D1
; CURRENT APPLICATION NUMBER: US/09/686,838B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/140,804
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/056,983
; PRIOR FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-686-838B-12
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-686-838B-12 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAACGACGG 16
RESULT 80
US-09-552-225A-19
; Sequence 19, Application US/09552225A
; Patent No. 6521233
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3
; FILE REFERENCE: 99-09
; CURRENT APPLICATION NUMBER: US/09/552,225A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-552-225A-19
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
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US-09-966-880A-8 (1-198) x US-09-552-225A-19 (1-18)

QY 32 ValValLysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 81
US-09-585-228-28
; Sequence 28, Application US/09585228
; Patent No. 6531576
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Burkhead, Steven K.
; TITLE OF INVENTION: FOUR-HELICAL BUNDLE PROTEIN ZS1G81
; FILE REFERENCE: 99-13
; CURRENT APPLICATION NUMBER: US/09/585,228
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: US 60/137,057
; EARLIER FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC976
US-09-585-228-28

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-585-228-28 (1-18)

QY 32 ValValLysArgArg 36
Db 2 GTTGTAACGACGG 16

RESULT 82
US-09-422-978-6619
; Sequence 6619, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6619
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-14074 for SEQ 2685,
US-09-422-978-6619

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Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-6619 (1-18)

QY 102 ProAsnLeuSerLeu 106
Db 4 CCAATCTATCCCTC 18

RESULT 83
US-09-422-978-10343
; Sequence 10343, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-11248 for SEQ 2478, in complen
US-09-422-978-10343

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-422-978-10343 (1-18)

QY 34 LysArgArgAspSer 38
Db 4 AAGAGACGAGACTCC 18

RESULT 84
US-09-404-641-6
; Sequence 6, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23

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; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-404-641-6

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-404-641-6 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
|||||

RESULT 85
US-09-923-246-77
; Sequence 77, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,504
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-923-246-77

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-923-246-77 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
|||||

RESULT 86
US-09-786-606-18
; Sequence 18, Application US/09786606
; Patent No. 6613547
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; APPLICANT: Raymond, Christopher K.
; APPLICANT: Vanaja, Erica
; APPLICANT: Miller, Brady G.
; APPLICANT: Sloan, James S.
; TITLE OF INVENTION: PICHIA METHANOLICA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 1
; FILE REFERENCE: PROMOTER AND TERMINATOR
; FILE REFERENCE: 98-56PC
; CURRENT APPLICATION NUMBER: US/09/786,606
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/140,703
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-09-786-606-18

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-786-606-18 (1-18)

QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
|||||

RESULT 87
US-09-552-204A-19
; Sequence 19, Application US/09552204A
; Patent No. 6620909
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
; FILE REFERENCE: 99-08
; CURRENT APPLICATION NUMBER: US/09/552,204A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,207
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC976
US-09-552-204A-19
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-552-204A-19 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 88
US-10-295-723-77
; Sequence 77, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; TYPE: DNA
; LENGTH: 18
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC976
US-10-295-723-77
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-10-295-723-77 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 89
PCT-US93-08174-2
; Sequence 2, Application PC/TUS9308174
; GENERAL INFORMATION:
; APPLICANT: NAME: ZymoGenetics, Inc.
; APPLICANT: STREET: 4225 Roosevelt Way North East
; APPLICANT: CITY: Seattle, Washington
; APPLICANT: COUNTRY: United States
; APPLICANT: POSTAL CODE: 98105
; APPLICANT: TELEPHONE: (206) 547-80808
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08174
; FILING DATE: 30-AUG-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ZC976
PCT-US93-08174-2
Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0
US-09-966-880A-8 (1-198) x PCT-US93-08174-2 (1-18)
Qy 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 90
PCT-US95-04063-172
; Sequence 172, Application PC/TUS9504063
; GENERAL INFORMATION:
; APPLICANT: HERNSTADT, CORINNA
; APPLICANT: PARKER, WILLIAM D.
; APPLICANT: DAVIS, ROBERT
; APPLICANT: MILLER, SCOTT W.
; TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
; TITLE OF INVENTION: Animal Models for Diseases Associated With Mitochondrial
; TITLE OF INVENTION: Defects
; NUMBER OF SEQUENCES: 206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04063-172

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US95-04063-172 (1-18)

QY 125 GlyLeuArgArgLeu 129
Db 2 GGTCTACGGAGGCTC 16

RESULT 91
5262866-10
Patent No. 5262866
APPLICANT: FRITSCH, EDWARD F.; COLLINS, MARY
TITLE OF INVENTION: PROCESS AND NUCLEIC ACID CONSTRUCT FOR
PRODUCING REAGENT COMPLEXES USEFUL IN DETERMINING TARGET
NUCLEOTIDE SEQUENCES
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
FILING DATE: 11-APR-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 729,504
FILING DATE: 02-MAY-1985
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
APPLICATION NUMBER: 684,308
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 684,305
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
SEQ ID NO: 10:
LENGTH: 18

Alignment Scores:
Pred. No.: 1e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x 5262866-10 (1-18)

QY 32 ValVallyLysArgArg 36
Db 2 GTTGTAAAACGACGG 16

RESULT 92
US-08-070-328A-17/C
Sequence 17, Application US/08070328A
Patent No. 5491225
GENERAL INFORMATION:
APPLICANT: Picone, Teresa
APPLICANT: McCallum, Theresa
APPLICANT: Zoccoli, Michael
TITLE OF INVENTION: PCR PRIMERS FOR DETECTION OF
LEGIONELLA SPECIES AND
METHODS FOR CONTROLLING
TITLE OF INVENTION: VISUAL INTENSITY IN NUCLEIC
ACID HYBRIDIZATION ASSAYS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,328A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stas, Stacey R., Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8784
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
US-08-070-328A-17

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-070-328A-17 (1-19)

QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 93
US-08-146-504-21
Sequence 21, Application US/08146504
Patent No. 5605662
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING

;; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
;; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/146,504
;; FILING DATE: No. 5605662ember 1, 1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 203/218
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-146-504-21
;;
Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-146-504-21 (1-19)
QY 56 HisValGluLeuLeu 60
DB 2 CACGTAGACTGCTC 16
RESULT 94
US-08-455-116-17/c
; Sequence 17, Application US/08455116
; Patent No. 5614388
; GENERAL INFORMATION:
; APPLICANT: Picone, Teresa
; APPLICANT: McCallum, Theresa
; APPLICANT: Zoccoli, Michael
; TITLE OF INVENTION: PCR PRIMERS FOR DETECTION OF LEGIONELLA
; TITLE OF INVENTION: SPECIES AND METHODS FOR CONTROLLING VISUAL
; TITLE OF INVENTION: INTENSITY IN NUCLEIC ACID HYBRIDIZATION
; TITLE OF INVENTION: ASSAYS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey

;; COUNTRY: USA
;; ZIP: 07110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.24
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,116
;; FILING DATE: May 31, 1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Petty, Douglas A., Ph.D.
;; REGISTRATION NUMBER: 35,321
;; REFERENCE/DOCKET NUMBER: 9177
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (510) 814-2974
;; TELEFAX: (510) 814-2977
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (probe)
;; US-08-455-116-17
;;
Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-455-116-17 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGACTGCTC 4
RESULT 95
US-08-154-019-20
; Sequence 20, Application US/08154019
; Patent No. 5633076
; GENERAL INFORMATION:
; APPLICANT: Deboer, Herman A.
; APPLICANT: Strijker, Rein
; APPLICANT: Heyneker, Herbert L.
; APPLICANT: Platenburg, Gerald
; APPLICANT: Lee, Sang He
; APPLICANT: Pieper, Frank
; APPLICANT: Krimpenfort, Paul J.A.
; TITLE OF INVENTION: Production of Recombinant Polypeptides
; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154,019
; FILING DATE: 16-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/461,333
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-154-019-20

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-154-019-20 (1-19)
Qy 32 ValVallyatqArg 36
Db 5 GTTGTAACGACGG 19

RESULT 96
US-08-634-331-15/c
Sequence 15, Application US/08634331
Patent No. 5707809
GENERAL INFORMATION:
APPLICANT: HALVERSON, Joy L.
TITLE OF INVENTION: AVIAN SEX IDENTIFICATION PROBES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,331
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-55362-3/BIR/PJS
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 2777299FHT UR
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer"
US-08-634-331-15

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-634-331-15 (1-19)
Qy 82 ThrSerTprSerPro 86
Db 17 ACAAGCTGGAGCCCA 3

RESULT 97
US-08-295-743-18/c
Sequence 18, Application US/08295743
Patent No. 5719271
GENERAL INFORMATION:
APPLICANT: ISIS Pharmaceuticals, Inc.
TITLE OF INVENTION: Covalently Cross-Linked
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5719271ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,743
FILING DATE: 30-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 846,376
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 2'-O-[propion-3-yl bis(o-

OTHER INFORMATION: nitrobenzyl) acetal] group
FEATURE:
NAME/KEY: Modified-site
LOCATION: 17
OTHER INFORMATION: 2'-O-[propion-3-al bis(o-
OTHER INFORMATION: nitrobenzyl) acetal] group
US-08-295-743-18

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880a-8 (1-198) x US-08-295-743-18 (1-19)

OY 179 IleLeuLeuProLeu 183
Db 17 ATTCTCTACTCTTG 3

RESULT 98
US-08-461-333-20
Sequence 20, Application US/08461333
Patent No. 5741957
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,333
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003123
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-461-333-20

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880a-8 (1-198) x US-08-461-333-20 (1-19)

OY 32 ValVallysAIGaIG 36
Db 5 GTTGTAAACGACGG 19

RESULT 99
US-08-534-454-2
Sequence 2, Application US/08534454
Patent No. 5849486
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; O'Connell, James P.; Juncosa, Robert D.; Soano
TITLE OF INVENTION: APPARATUS AND METHODS FOR ACTIVE
TITLE OF INVENTION: PROGRAMMABLE MATRIX DEVICES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS (VERSION 3.0)
SOFTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,454
FILING DATE: September 27, 1995
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,657
FILING DATE: September 9, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 216/054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-534-454-2

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-534-454-2 (1-19)

QY 56 HisValGluLeuLeu 60
 |||||
 Db 2 CACGTAGAACTGCTC 16

RESULT 100

US-08-725-976-21

; Sequence 21, Application US/08725976

; Patent No. 5929208

; GENERAL INFORMATION:

; APPLICANT: Heller, Michael J.; and Tu, Eugene

; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb

; COMPUTER: IBM compatible

; OPERATING SYSTEM: WINDOWS (VERSION 3.0)

; SOFTWARE: WordPerfect (Version 6.0)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/725,976

; FILING DATE: October 4, 1996

; CLASSIFICATION: 422

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/146,504

; FILING DATE: No. 5929208ember 1, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Murphy, David B.

; REGISTRATION NUMBER: 31,125

; REFERENCE/DOCKET NUMBER: 222/211

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-725-976-21

Alignment Scores:
 Pred. No.: 1.06e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-725-976-21 (1-19)

QY 56 HisValGluLeuLeu 60
 |||||
 Db 2 CACGTAGAACTGCTC 16

RESULT 101

US-08-464-167-20

; Sequence 20, Application US/08464167

; Patent No. 6013857

; GENERAL INFORMATION:

; APPLICANT: Deboer, Herman A.

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Strijker, Rein

; APPLICANT: Heyneker, Herbert L.
 ; APPLICANT: Platenburg, Gerald
 ; APPLICANT: Lee, Sang He
 ; APPLICANT: Pieper, Frank
 ; APPLICANT: Krampenfort, Paul J.A.
 ; TITLE OF INVENTION: Production of Recombinant Polypeptides
 ; TITLE OF INVENTION: by Bovine Species and Transgenic Methods
 ; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,167

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,788

; FILING DATE: 15-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/895,956

; FILING DATE: 15-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/619,131

; FILING DATE: 27-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/444,745

; FILING DATE: 01-DEC-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebescheutz, Joe O.

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 16994-003124

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-543-3600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-464-167-20

Alignment Scores:
 Pred. No.: 1.06e+03 Length: 19
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.53% Indels: 0
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-464-167-20 (1-19)

QY 32 ValValLysArgArg 36
 |||||
 Db 5 GTTGTAACGACGG 19

RESULT 102

US-08-271-882B-21

; Sequence 21, Application US/08271882B

; Patent No. 6017696

; GENERAL INFORMATION:

; APPLICANT: Michael J. Heller

; ATTORNEY/AGENT INFORMATION:

; APPLICANT: Eugene Tu

```

; APPLICANT: Glen A. Evans
; APPLICANT: Ronald G. Sosnowski
; TITLE OF INVENTION: SELF-ADDRESSABLE
; TITLE OF INVENTION: SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND
; TITLE OF INVENTION: DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS
; TITLE OF INVENTION: AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/05/271,882B
; FILING DATE: July 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 6017696ember 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 207/263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic
; TYPE: acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-882B-21

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-271-882B-21 (1-19)

QY 56 HisValGluLeuLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 103
US-08-855-058-2
; Sequence 2, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175

```

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; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
; OTHER INFORMATION: probe
; US-08-855-058-2

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-2 (1-19)

QY 56 HisValGluLeuLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 104
US-08-855-058-8
; Sequence 8, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
; US-08-855-058-8

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-8 (1-19)

QY 56 HisValGluLeuLeu 60
DB 2 CACGTAGAACTGCTC 16

RESULT 105
US-08-855-058-9/c
; Sequence 9, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.

```

```
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-9

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-9 (1-19)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAGCTGCTC 4

RESULT 106
US-08-855-058-10/c
; Sequence 10, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-10

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-10 (1-19)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAGCTGCTC 4

RESULT 107
US-08-855-058-11/c
; Sequence 11, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
```

```
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-11

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-11 (1-19)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 108
US-08-855-058-12/c
; Sequence 12, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Sosnowski, Ronald G.
; APPLICANT: O'Connell, James P.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
; TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
; TITLE OF INVENTION: SYNTHESIS
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
; CURRENT APPLICATION NUMBER: US/08/855,058A
; CURRENT FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Human HLA
US-08-855-058-12

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-12 (1-19)
Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 109
US-08-855-058-13/c
; Sequence 13, Application US/08855058A
; Patent No. 6048690
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
```


APPLICANT: Sosnowski, Ronald G.
APPLICANT: O'Connell, James P.
TITLE OF INVENTION: METHODS FOR ELECTRONIC FLUORESCENT PERTURBATION FOR
TITLE OF INVENTION: ANALYSIS AND ELECTRONIC PERTURBATION CATALYSIS FOR
TITLE OF INVENTION: SYNTHESIS
FILE REFERENCE: DAVID B. MURPHY: Nanogen 224/175
CURRENT APPLICATION NUMBER: US/08/855,058A
CURRENT FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 19
TYPE: DNA
ORGANISM: Human HLA
US-08-855-058-13

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-855-058-13 (1-19)

Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 110
US-09-158-313-20
Sequence 20, Application US/09158313
Patent No. 6066725
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,313
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989

ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16994-003125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-158-313-20

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-158-313-20 (1-19)

Qy 32 ValVallysArgArg 36
Db 5 GTTGTAACGACGG 19

RESULT 111
US-08-476-798-20
Sequence 20, Application US/08476798
Patent No. 6140552
GENERAL INFORMATION:
APPLICANT: Deboer, Herman A.
APPLICANT: Strijker, Rein
APPLICANT: Heyneker, Herbert L.
APPLICANT: Platenburg, Gerald
APPLICANT: Lee, Sang He
APPLICANT: Pieper, Frank
APPLICANT: Krimpenfort, Paul J.A.
TITLE OF INVENTION: Production of Recombinant Polypeptides
TITLE OF INVENTION: by Bovine Species and Transgenic Methods
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,798
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,788
FILING DATE: 15-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/895,956
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,131
FILING DATE: 27-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/444,745
FILING DATE: 01-DEC-1989

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16994-003125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-476-798-20

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-476-798-20 (1-19)

QY 32 ValVallysArgArg 36
Db 5 GTTGTAACCGCG 19

RESULT 112
US-08-726-278-21
; Sequence 21, Application US/08726278
; Patent No. 6238624
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Evans, Glen A.
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR
; FILE REFERENCE: DAVID B. MURPHY/NANOGEN: 222-210
; CURRENT FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: US/08/726,278
; PRIOR FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for
; OTHER INFORMATION: Labeling
US-08-726-278-21

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-726-278-21 (1-19)

QY 56 HisValGluLeu 60
Db 2 CACGTAGACTGCTC 16

RESULT 113
US-09-141-286-2
; Sequence 2, Application US/09141286
; Patent No. 6245508
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; O'Connell, James P.; Juncosa,
; APPLICANT: Robert D.; Sosnowski, Ronald G.; Jackson, Thomas
; APPLICANT: R.
; TITLE OF INVENTION: METHOD FOR FINGERPRINTING UTILIZING
; TITLE OF INVENTION: AN ELECTRONICALLY ADDRESSABLE ARRAY
; TITLE OF INVENTION: (as amended)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon LLP
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,286
; FILING DATE: August 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/534,454
; FILING DATE: September 27, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 225/167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-141-286-2

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-141-286-2 (1-19)

QY 56 HisValGluLeu 60
Db 2 CACGTAGACTGCTC 16

RESULT 114
US-09-144-367-44
; Sequence 44, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
```

```
/ PRIOR FILING DATE: 1997-09-10
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 44
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: H. sapiens
US-09-144-367-44

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-144-367-44 (1-19)

Qy 22 LysGlyArgArgGlu 26
Db 3 AAGGCGAGGAGAG 17

RESULT 115
US-09-536-977-100
/ Sequence 100, Application US/09536977
/ Patent No. 6649409
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
/ TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
/ TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
/ TITLE OF INVENTION: BX08 CONSTRUCTS
/ FILE REFERENCE: 030307/0169
/ CURRENT APPLICATION NUMBER: US/09/536,977
/ CURRENT FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: 60/128,558
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: DK PA1999 00427
/ PRIOR FILING DATE: 1999-03-29
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 100
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-977-100

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-536-977-100 (1-19)

Qy 32 ValVallyArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 116
PCT-US93-02059-18/c
/ Sequence 18, Application PC/TUS9302059
/ GENERAL INFORMATION:
/ APPLICANT: David Ecker
/ TITLE OF INVENTION: Covalently Cross-linked
/ TITLE OF INVENTION: Oligonucleotides
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Woodcock Washburn Kurtz
/ ADDRESSEE: Mackiewicz & Norris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/02059
/ FILING DATE: 19930305
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 846,376
/ FILING DATE: March 5, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Joseph Lucci
/ REGISTRATION NUMBER: 33,307
/ REFERENCE/DOCKET NUMBER: ISIS-0980
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ ANTI-SENSE: no
PCT-US93-02059-18

Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US93-02059-18 (1-19)

Qy 179 IleLeuLeuProLeu 183
Db 17 ATTCTCTACCTCTG 3

RESULT 117
5455029-5/c
/ Patent No. 5455029
/ APPLICANT: HARTMAN, JACOB R.; OPPENHEIM, AMOS B.; GORECKI,
/ MARIAN; AVIV, HAIM; OREN, RACHEL
/ TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING
/ A MIXTURE OF HUMAN CUZIN SUPEROXIDE DISMUTASE ANALOGS
/ NUMBER OF SEQUENCES: 30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/933,500
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 449,125
/ FILING DATE: 08-DEC-1989
/ APPLICATION NUMBER: 202,238
/ FILING DATE: 03JUN-1988
/ APPLICATION NUMBER: 897,056
/ FILING DATE: 14-AUG-1985
/ APPLICATION NUMBER: 767,143
/ FILING DATE: 19-AUG-1985
/ APPLICATION NUMBER: 844,245
/ FILING DATE: 27-AUG-1984
/ SEQ ID NO: 5
/ LENGTH: 19
```

```

5455029-5
Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x 5455029-5 (1-19)

QY 69 AspleuAspProGly 73
DB 18 GATCTAGACCGGGA 4

RESULT 118
5455029-25/c
;PATENT NO. 5455029
; APPLICANT: HARTMAN, JACOB R.; OPPENHEIM, AMOS B.; GORECKI,
; MARIAN; AVIV, HAIM; OREN, RACHEL
; TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING
; A MIXTURE OF HUMAN CUZIN SUPEROXIDE DISMUTASE ANALOGS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/933,500
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 449,125
; FILING DATE: 08-DEC-1989
; APPLICATION NUMBER: 202,238
; FILING DATE: 03JUN-1988
; APPLICATION NUMBER: 897,056
; FILING DATE: 14-AUG-1985
; APPLICATION NUMBER: 767,143
; FILING DATE: 19-AUG-1985
; APPLICATION NUMBER: 644,245
; FILING DATE: 27-AUG-1984
; SEQ ID NO:25:
; LENGTH: 19
5455029-25
Alignment Scores:
Pred. No.: 1.06e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x 5455029-25 (1-19)

QY 69 AspleuAspProGly 73
DB 18 GATCTAGACCGGGA 4

RESULT 119
US-07-664-989B-104/c
; Sequence 104, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Lev, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.

```

```

; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
US-07-664-989B-104

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-664-989B-104 (1-20)

QY 178 ArgileuLeuPro 182
DB 18 CGGATCCTCCTCCT 4

RESULT 120
US-07-931-473B-59
; Sequence 59, Application US/07931473B
; Patent No. 5270163
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS

```

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; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/931.473B
; FILING DATE: 19920817
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-931-473B-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-931-473B-59 (1-20)
QY 32 ValVallysArgArg 36
Db 4 GTTGTAACGACGG 18

RESULT 121
US-07-714-131C-59
; Sequence 59, Application US/07714131C
; Patent No. 5475096
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 344
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/714.131C
; FILING DATE: June 10, 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
US-07-714-131C-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-714-131C-59 (1-20)
QY 32 ValVallysArgArg 36
Db 4 GTTGTAACGACGG 18

RESULT 122
US-07-872-678A-13/c
; Sequence 13, Application US/07872678A
; Patent No. 5541060
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme, et al.
; TITLE OF INVENTION: DETECTION OF EARLY-ONSET
; TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: Post Office Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,678A
; FILING DATE: 22-APRIL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: ARCD016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA ( Genomic)
US-07-872-678A-13

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-872-678A-13 (1-20)
QY 104 LeuSerLeuArgile 108
Db 18 TTGAGCCTCAGATC 4

```

RESULT 123
US-08-271-946A-20
; Sequence 20, Application US/08271946A
; Patent No. 5545527
; GENERAL INFORMATION:
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: Method for Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.946A
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-002-US
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 21 of human RBL gene
US-08-271-946A-20
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-271-946A-20 (1-20)
QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16
RESULT 124
US-08-271-942A-20
; Sequence 20, Application US/08271942A
; Patent No. 5550020
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.

APPLICANT: Dunn, James M.
APPLICANT: Stevens, John K.
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271.942A
FILING DATE: 08-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-003-US
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
NAME/KEY: primer for exon 21 of human RBL gene
US-08-271-942A-20
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-271-942A-20 (1-20)
QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16
RESULT 125
US-08-259-745A-47
; Sequence 47, Application US/08259745A
; Patent No. 5582983
; GENERAL INFORMATION:
; APPLICANT: Anderson, Donald
; APPLICANT: Schollin, Christopher
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS OF IDENTIFYING ALEXANDRIUM
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

```

; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,745A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/967,637
; FILING DATE: 28-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Neuner, George W.
; REGISTRATION NUMBER: 26,964
; REFERENCE/DOCKET NUMBER: 42,101 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-259-745A-47

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-259-745A-47 (1-20)

QY 170 ValArgLeuSerArg 174
Db 6 GTCCGTCCTTTCAAGA 20

RESULT 126
US-08-146-504-7/c
; Sequence 7, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM compatible

```

```

; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,504
; FILING DATE: No. 5605662ember 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 203/218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-146-504-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-146-504-7 (1-20)

QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 127
US-08-306-546C-3
; Sequence 3, Application US/08306546C
; Patent No. 5605797
; GENERAL INFORMATION:
; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,546C
; FILING DATE: September 15, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003

```

none

TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer
US-08-306-546C-3

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-306-546C-3 (1-20)

QY 179 IleLeuLeuProLeu 183
Db 6 ATTCTTTACCCCTG 20

RESULT 128
US-08-170-689-1
Sequence 1, Application US/08170689
Patent No. 5624798
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NOBUKO
APPLICANT: OKAMOTO, TADASHI
APPLICANT: TOMIDA, YOSHINORI
APPLICANT: MIYAZAKI, TAKESHI
APPLICANT: KAWAGUCHI, YASUHIRO
TITLE OF INVENTION: FLUORESCENT STAIN CONTAINING
TITLE OF INVENTION: OF PYLUMIN SALT OR ITS SIMILAR SALT, DETECTION METHOD
TITLE OF INVENTION: OF NUCLEIC ACID BY USE OF IT, AND FLUORESCENT
TITLE OF INVENTION: STAINING METHOD OF BIOLOGICAL SAMPLE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 277 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: UNITED STATES
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,689
FILING DATE: 21-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WOLLMAN, PENINA
REGISTRATION NUMBER: 30,816
REFERENCE/DOCKET NUMBER: 35.C9616
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-212-758-2400
TELEFAX: 1-212-758-2982
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-170-689-1

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-170-689-1 (1-20)

QY 32 ValVallysArgArg 36
Db 1 GTTGTAACGACGG 15

RESULT 129
US-08-412-110-59
Sequence 59, Application US/08412110
Patent No. 5670637
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,110
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-412-110-59 (1-20)

QY 32 ValVallysArgArg 36
Db 4 GTTGTAACGACGG 18

RESULT 130
US-08-317-872A-1
; Sequence 1, Application US/08317872A
; Patent No. 5679516
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: MIYAZAKI, TAKESHI
; TITLE OF INVENTION: PROCESS FOR DETECTING NUCLEIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 277 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10172-0174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,872A
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXON, PETER
; REGISTRATION NUMBER: 24,947
; REFERENCE/DOCKET NUMBER: 35C10188
; TELEPHONE: 1-212-758-2400
; TELEFAX: 1-212-758-2982
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (SYNTHESIZED POLYNUCLEOTIDE)
US-08-317-872A-1
Alignment Scores:
Pred. No.: 1-11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-317-872A-1 (1-20)
Qy 32 ValVallysargArg 36
Db 1 GTTGTAACGACGG 15
RESULT 131
US-08-317-872A-2/c
; Sequence 2, Application US/08317872A
; Patent No. 5679516
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: MIYAZAKI, TAKESHI
; TITLE OF INVENTION: PROCESS FOR DETECTING NUCLEIC ACID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 277 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10172-0174
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,872A
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SAXON, PETER
REGISTRATION NUMBER: 24,947
REFERENCE/DOCKET NUMBER: 35C10188
TELEPHONE: 1-212-758-2400
TELEFAX: 1-212-758-2982
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (SYNTHESIZED POLYNUCLEOTIDE)
US-08-317-872A-2
Alignment Scores:
Pred. No.: 1-11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-317-872A-2 (1-20)
Qy 32 ValVallysargArg 36
Db 20 GTTGTAACGACGG 6
RESULT 132
US-08-255-892-36
; Sequence 36, Application US/08255892
; Patent No. 5695926
; GENERAL INFORMATION:
; APPLICANT: CROS, PHILIPPE
; APPLICANT: ALLIBERT, PATRICE
; APPLICANT: MALLEET, FRANCOIS
; APPLICANT: MABILAT, CLAUDE
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: PROCEDURE FOR DETECTION OF A NUCLEOTIDE
; TITLE OF INVENTION: SEQUENCE BY IMPLEMENTING THE SANDWICH HYBRIDIZATION
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,892
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/834,543
; FILING DATE: 11-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.

```
; ; REGISTRATION NUMBER: 23,048
; ; REFERENCE/DOCKET NUMBER: 1032/94109
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 202-861-3000
; ; TELEFAX: 202-822-0944
; ; TELEX: 6714627 CUSH
; ; INFORMATION FOR SEQ ID NO: 36:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 20 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: DNA (genomic)
; ; US-08-255-892-36

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-255-892-36 (1-20)

QY 174 ArginLeuArgArg 178
Db 1 AGACAGCTCAGAAGA 15

RESULT 133
US-08-409-442A-59
; Sequence 59, Application US/08409442A
; Patent No. 5696249
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,442A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-409-442A-59
```

```
; ; REGISTRATION NUMBER: 35,095
; ; REFERENCE/DOCKET NUMBER: 1032/94109
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 202-861-3000
; ; TELEFAX: 202-822-0944
; ; TELEX: 6714627 CUSH
; ; INFORMATION FOR SEQ ID NO: 36:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 20 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: DNA (genomic)
; ; US-08-255-892-36

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-409-442A-59 (1-20)

QY 32 ValVallysArgArg 36
Db 4 GTTGTAAACGACGG 18

RESULT 134
US-08-671-829-1
; Sequence 1, Application US/08671829
; Patent No. 5705346
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: TOMIDA, YOSHINORI
; APPLICANT: YAMAMOTO, NOBUKO
; APPLICANT: KAWAGUCHI, MASAHIRO
; APPLICANT: MAKINO, KEISUKE
; APPLICANT: MURAKAMI, AKIRA
; TITLE OF INVENTION: METHOD FOR DETECTING TARGET
; TITLE OF INVENTION: NUCLEIC ACID
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 277 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,829
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/157,427
; FILING DATE: 26-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wollman, Penina
; REGISTRATION NUMBER: 30,816
; REFERENCE/DOCKET NUMBER: 35.C9569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-2400
; TELEFAX: 212-758-2982
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-671-829-1

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-671-829-1 (1-20)
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QY 32 ValVallyeArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 135
US-08-555-678-49/c
; Sequence 49, Application US/08555678
; Patent No. 5763174
; GENERAL INFORMATION:
; APPLICANT: Nishikura, Kazuko
; TITLE OF INVENTION: RNA Editing Enzyme and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,678
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,794
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/280,443
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,459
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST49DUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"

US-08-555-678-49

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Db: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-555-678-49 (1-20)

QY 38 SerAlaThrSerPhe 42
Db 17 TCAGCCACATCCTC 3

RESULT 136
US-08-753-147-100
; Sequence 100, Application US/08753147

Patent No. 5770372
; GENERAL INFORMATION:
; APPLICANT: Concannon, Patrick
; TITLE OF INVENTION: Detection of Mutations in the Human ATM Gene
; NUMBER OF SEQUENCES: 196
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson and Kindness
; STREET: 1420 5th Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,147
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: VMRC-1-9714
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 743-4387
; TELEFAX: (206) 224 0779
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-08-753-147-100

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
Db: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-753-147-100 (1-20)

QY 97 PheLeuArgGlyAsn 101
Db 4 TTTCTTAGAGGAAT 18

RESULT 137
US-08-464-531-44/c
; Sequence 44, Application US/08464531
; Patent No. 5789184
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,531
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKS=2G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-464-531-44

```

```

Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-464-531-44 (1-20)

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QY 104 LeuSerLeuArgile 108
Db 18 CTGAGTCCTCGCATC 4

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RESULT 138
US-08-530-524A-3
; Sequence 3, Application US/08530524A
; Patent No. 5837836
; GENERAL INFORMATION:
; APPLICANT: Priderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan

```

```

; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,524A
; FILING DATE: September 19, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003DVA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-530-524A-3

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Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-530-524A-3 (1-20)

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QY 179 IleLeuLeuProleu 183
Db 6 ATTCTTTACCCCTG 20

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RESULT 139
US-08-467-007A-2
; Sequence 2, Application US/08467007A
; Patent No. 5840875
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Meyer, Timothy W.
; APPLICANT: Oberbauer, Rainer
; TITLE OF INVENTION: Method For Administering Antisense
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,007A
; FILING DATE: 06/06/95
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 95,728
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000

```

TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-467-007A-2
Alignment Scores: 1.11e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-467-007A-2 (1-20)
QY 102 ProAsnLeuSerLeu 106
Db 5 CCCATCTCTCGCTG 19
RESULT 140
US-08-469-609A-59
; Sequence 59, Application US/08469609A
; Patent No. 5843653
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,609A
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; FILING DATE: April 25, 1995
; APPLICATION NUMBER: 08/428,964
; PRIOR APPLICATION DATA:
; FILING DATE: March 27, 1995
; APPLICATION NUMBER: 08/412,110
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C5
; TELEPHONE: (303) 793-3333
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-609A-59
Alignment Scores: 1.11e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 2 Gaps: 0
US-09-966-880A-8 (1-198) x US-08-469-609A-59 (1-20)
QY 32 ValVallysArgArg 36
Db 4 GTTGTAAACGACGG 18
RESULT 141
US-08-117-952-475/C
; Sequence 475, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 475:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-117-952-475
Alignment Scores: 1.11e+03 Length: 20
Pred. No.: 5.00 Matches: 5
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
DB: 2 Gaps: 0

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US-09-966-880A-8 (1-198) x US-08-117-952-475 (1-20)
QY 127 ArgatgLeuHisarg 131
Db 18 AGAGAGCTGCACAGA 4

RESULT 142
US-08-117-952-646/c
; Sequence 646, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 646:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-117-952-646

Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-117-952-646 (1-20)
QY 57 ValgluLeuPhe 61
Db 18 GTTGAGCTGCTTC 4

RESULT 143
US-08-461-598-44/c
; Sequence 44, Application US/08461598
; Patent No. 5876951
; GENERAL INFORMATION:

```

```

; APPLICANT: FOLWKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/461,598
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/322,137
; FILING DATE: 13-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES-2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-461-598-44

Alignment Scores:
Pred. No.: 1,11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-461-598-44 (1-20)
QY 104 LeuSerLeuArgile 108
Db 18 CTGAGTCTTCGATC 4

RESULT 144
US-08-832-658A-5
; Sequence 5, Application US/08832658A
; Patent No. 5914269

```

;; GENERAL INFORMATION:
;; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
;; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF EPIDERMAL
;; TITLE OF INVENTION: GROWTH FACTOR RECEPTOR EXPRESSION
;; NUMBER OF SEQUENCES: 7
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5914269ris LLP
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: U.S.A.
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/832,658A
;; FILING DATE: April 4, 1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Paul K. Legaard
;; REGISTRATION NUMBER: 38,534
;; REFERENCE/DOCKET NUMBER: ISIS-2450
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-832-658A-5

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-832-658A-5 (1-20)

Qy 129 LeuHisArgAlaGly 133
Db 6 TTGCACAGGGCAGGG 20

RESULT 145

;; US-08-725-976-7/c
;; Sequence 7, Application US/08725976
;; Patent No. 5929208
;; GENERAL INFORMATION:
;; APPLICANT: Heller, Michael J.; and Tu, Eugene
;; TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: WINDOWS (VERSION 3.0)
;; SOFTWARE: WordPerfect (Version 6.0)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/725,976
;; FILING DATE: October 4, 1996

;; CLASSIFICATION: 422
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: 08/146,504
;; FILING DATE: No. 5929208ember 1, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murthy, David B.
;; REGISTRATION NUMBER: 31,125
;; REFERENCE/DOCKET NUMBER: 222/211
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEFAX: 67-3510
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-725-976-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-725-976-7 (1-20)

Qy 56 HisValGluLeuLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 146

;; US-08-683-918-1
;; Sequence 1, Application US/08683918
;; Patent No. 5939256
;; GENERAL INFORMATION:
;; APPLICANT: YAMAMOTO, NUBUKO
;; APPLICANT: OKAMOTO, TADASHI
;; APPLICANT: TOMIDA, YOSHINORI
;; APPLICANT: KAWAGUCHI, MASAHITO
;; APPLICANT: MAKINO, KEISUKE
;; APPLICANT: MURAKAMI, AKIRA
;; TITLE OF INVENTION: METHOD FOR DETECTION OF NUCLEIC
;; TITLE OF INVENTION: ACID AND PROBE THEREFOR
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
;; STREET: 277 Park Avenue
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 10172-0194
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/683,918
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/157,318
;; FILING DATE: 26-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WOLLMAN, PENINA
;; REGISTRATION NUMBER: 30,816
;; REFERENCE/DOCKET NUMBER: 35.C9568

; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,882B
; FILING DATE: July 7, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,504
; FILING DATE: No. 6017696member 1, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, David B.
; REGISTRATION NUMBER: 31,125
; REFERENCE/DOCKET NUMBER: 207/263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-271-882B-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-271-882B-7 (1-20)
QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 150
US-08-782-798-1
; Sequence 1, Application US/08782798
; Patent No. 6022961
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, NOBUKO
; APPLICANT: OKAMOTO, TADASHI
; APPLICANT: TOMIDA, YOSHINORI
; APPLICANT: MIYAZAKI, TAKESHI
; APPLICANT: KAWAGUCHI, MASAHIRO
; TITLE OF INVENTION: FLUORESCENT STAIN CONTAINING
; TITLE OF INVENTION: PYRYLIUM SALT OR ITS SIMILAR SALT, DETECTION METHOD
; TITLE OF INVENTION: OF NUCLEIC ACID BY USE OF IT, AND FLUORESCENT
; NUMBER OF INVENTION: STAINING METHOD OF BIOLOGICAL SAMPLE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 277 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: UNITED STATES
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,798
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/170,689
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WOLLMAN, PENINA
; REGISTRATION NUMBER: 30,816
; REFERENCE/DOCKET NUMBER: 35.C9616 DIV.I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-212-758-2400
; TELEFAX: 1-212-758-2982
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SYNTHETIC DNA"
US-08-782-798-1

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-782-798-1 (1-20)
QY 32 ValVallylsArgArg 36
Db 1 GTTGTAAACGACGG 15

RESULT 151
US-08-779-916A-20
; Sequence 20, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 21 of human RBL gene
US-08-779-916A-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-779-916A-20 (1-20)

QY 28 TyrLeuCysTyrVal 32
DB 2 TACCTATGTTATGTT 16

RESULT 152
US-08-777-266A-69
; Sequence 69, Application US/08777266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20

```

```

; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-777-266A-69

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-777-266A-69 (1-20)

QY 176 LeuAtcAtgIleleu 180
DB 1 CTGCGCCGAATCCTG 15

RESULT 153
US-08-322-137-44/c
; Sequence 44, Application US/08322137
; Patent No. 6100042
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BROACH, Jim
; APPLICANT: MANFREDI, John
; APPLICANT: KLEIN, Christine
; APPLICANT: MURPHY, Andrew J.
; APPLICANT: PAUL, Jeremy
; APPLICANT: TRUEHEART, Joshua
; TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
; TITLE OF INVENTION: PHORMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/322,137
; FILING DATE: 13-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,313
; FILING DATE: 20-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,328
; FILING DATE: 31-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,431
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOLWKES=2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-322-137-44

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-322-137-44 (1-20)
QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGCATC 4

RESULT 154
US-09-143-190-59
; Sequence 59, Application US/09143190
; Patent No. 6110900
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Turk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,190
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

US-09-143-190-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-143-190-59 (1-20)
QY 32 valvallyysargArg 36
Db 4 GTTGTAAACGACGG 18

RESULT 155
US-08-600-982-20/c
; Sequence 20, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,982
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: PCR primer; see TABLE 1
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-600-982-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-600-982-20 (1-20)
QY 59 LeuLeuPheLeuArg 63

```

DB 19 TTGCTATTCTCAGA 5
RESULT 156
US-09-418-641-39
; Sequence 39, Application US/09418641A
; Patent No. 6124133
; GENERAL INFORMATION:
; APPLICANT: Jennifer K. Taylor
; APPLICANT: Lex M. Coweert
; TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
; FILE REFERENCE: RTS-0105
; CURRENT APPLICATION NUMBER: US/09/418.641A
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-641-39
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-418-641-39 (1-20)
QY 59 LeuLeuPheLeuArg 63
DB 6 CTCCTCTTCCTCCGG 20
RESULT 157
US-09-069-886-34
; Sequence 34, Application US/09069886
; Patent No. 6132724
; GENERAL INFORMATION:
; APPLICANT: Blum, Kenneth
; APPLICANT: Comings, David E.
; APPLICANT: Ivy, John L.
; TITLE OF INVENTION: ALLELIC POLYGENE DIAGNOSIS OF REWARD
; TITLE OF INVENTION: DEFICIENCY SYNDROME AND TREATMENT
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,886
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: BLUM:002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512)418-3000
; TELEFAX: (512)474-7577
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-069-886-34
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-069-886-34 (1-20)
QY 22 LysGlyArgArgGlu 26
DB 5 AAGGGAAGGAGGAA 19
RESULT 158
US-09-428-584-14
; Sequence 14, Application US/09428584
; Patent No. 6136604
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF METHIONINE AMINOPEPTIDASE 2 EXPRESSION
; FILE REFERENCE: RTS-0114
; CURRENT APPLICATION NUMBER: US/09/428,584
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-584-14
Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-428-584-14 (1-20)
QY 70 LeuAspProGlyArg 74
DB 6 CTGGATCCAGGTGCG 20
RESULT 159
US-08-882-046-31/c
; Sequence 31, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Krantz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UW 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..10
; FEATURE:
; NAME/KEY: intron
; LOCATION: 11..20
US-08-882-046-31

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-882-046-31 (1-20)

QY 27 ThrTyrLeuCysTyr 31
Db 16 ACATACCTCTGTAC 2

RESULT 160
US-09-444-053-19/c
; Sequence 19, Application US/09444053A
; Patent No. 6165728
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
; FILE REFERENCE: RTS-0122
; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-19

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-444-053-19 (1-20)

QY 27 ThrTyrLeuCysTyr 31
Db 16 ACATACCTCTGTAC 2

RESULT 160
US-09-444-053-19/c
; Sequence 19, Application US/09444053A
; Patent No. 6165728
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
; FILE REFERENCE: RTS-0122
; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-19

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-444-053-19 (1-20)

QY 27 ThrTyrLeuCysTyr 31
Db 16 ACATACCTCTGTAC 2
```

```
QY 163 GluGlyLeuHisGlu 167
Db 15 GAAGGACTCCATGAA 1

RESULT 161
US-09-444-053-20/c
; Sequence 20, Application US/09444053A
; Patent No. 6165728
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
; FILE REFERENCE: RTS-0122
; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-444-053-20 (1-20)

QY 163 GluGlyLeuHisGlu 167
Db 20 GAAGGACTCCATGAA 6

RESULT 162
US-09-433-694-63
; Sequence 63, Application US/09433694
; Patent No. 6165790
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P55 GAMMA EXPRESSION
; FILE REFERENCE: RTS-0098
; CURRENT APPLICATION NUMBER: US/09/433,694
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-694-63

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-433-694-63 (1-20)

QY 29 LeuCysTyrValVal 33
Db 3 CTTTGTATGTTGTT 17
```

RESULT 163

US-09-435-296-73
; Sequence 73, Application US/09435296
; Patent No. 6171860

; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker

; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF RANK EXPRESSION

; FILE REFERENCE: RTS-0116
; CURRENT APPLICATION NUMBER: US/09/435,296

; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 73
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-435-296-73

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-435-296-73 (1-20)

QY 128 ArgLeuHisArgAla 132

DB 2 AGGCTGACCGGCT 16

RESULT 164

US-09-306-876A-7

; Sequence 7, Application US/09306876A
; Patent No. 6187595

; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank

; APPLICANT: Lipton, Allan
; APPLICANT: Witters, Lois M

; TITLE OF INVENTION: Oligonucleotide Inhibition of Epidermal Growth Factor

; FILE REFERENCE: Receptor Expression
; CURRENT APPLICATION NUMBER: US/09/306,876A

; CURRENT FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 08/832,658

; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: No. 6187595e1
; OTHER INFORMATION: Sequence

US-09-306-876A-7

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-306-876A-7 (1-20)

QY 129 LeuHisArgAlaGly 133

|||||

DB 6 TTGCACAGGGCAGG 20

RESULT 165

US-09-234-434-2/c

; Sequence 2, Application US/09234434
; Patent No. 6197532

; GENERAL INFORMATION:
; APPLICANT: Rao, Prakash N. et al.

; TITLE OF INVENTION: Diagnosis and Detection of Breast Cancer and Other

; FILE REFERENCE: Rao 9706M.1
; CURRENT APPLICATION NUMBER: US/09/234,434

; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/122,048

; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PCT primer
US-09-234-434-2

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-234-434-2 (1-20)

QY 179 IleLeuLeuProLeu 183

DB 19 ATCTCTCGCTCTG 5

RESULT 166

US-09-446-504-67

; Sequence 67, Application US/09446504
; Patent No. 6218150

; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi

; APPLICANT: SATO, Yoshimi
; APPLICANT: FUJITA, Tomoko

; APPLICANT: MIYAKE, Kazuo
; APPLICANT: MUKAI, Hiroyuki

; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin

; TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS
; FILE REFERENCE: 1422-408PCT

; CURRENT APPLICATION NUMBER: US/09/446,504
; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26

; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27

; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 67
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

US-09-446-504-67

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
------------	----------	---------	----

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-446-504-67 (1-20)

Qy 156 GluArgThrPheIys 160
Db 3 GAGAGAACTTCAAG 17

RESULT 167

US-08-726-278-7/c
; Sequence 7, Application US/08726278
; Patent No. 6238624
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.
; APPLICANT: Tu, Eugene
; APPLICANT: Evans, Glen A.
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS FOR ELECTRONIC TRANSPORT IN MOLECULAR
; FILE REFERENCE: BIOLOGICAL ANALYSIS AND DIAGNOSTICS 222-210
; CURRENT APPLICATION NUMBER: US/08/726,278
; PRIOR FILING DATE: 1996-10-04
; PRIOR APPLICATION NUMBER: 08/271,882
; PRIOR FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequences for
; OTHER INFORMATION: Labeling
US-08-726-278-7

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-726-278-7 (1-20)

Qy 56 HisValGluLeu 60
Db 18 CACGTAGACTGCTC 4

RESULT 168

US-09-437-239
; Sequence 239, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Anti-sense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
; EARLIER FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 239
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid
US-09-180-437-239

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-180-437-239 (1-20)

Qy 169 SerValArgLeuSer 173
Db 4 AGTGTCAAGTTATCC 18

RESULT 169

US-08-582-333A-47/c
; Sequence 47, Application US/08582333A
; Patent No. 6255059
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,333A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine J. Kara
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPI-012CPS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-582-333A-47

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-582-333A-47 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGATC 4

RESULT 170
US-08-582-333A-49/C
; Sequence 49, Application US/08582333A
; Patent No. 6255059
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J. M.
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Identifying Receptor Effectors
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582.333A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine J. Kara
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: CPT-012CP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-582-333A-49

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-582-333A-49 (1-20)

QY 104 LeuSerLeuArgIle 108
Db 18 CTGAGTCTTCGATC 4

RESULT 171
US-08-875-243-4
; Sequence 4, Application US/08875243
; Patent No. 6255475
; GENERAL INFORMATION:
; APPLICANT: KWIAKOWSKI, Marek
; TITLE OF INVENTION: NOVEL CHAIN TERMINATORS, THE USE THEREOF FOR NUCLEIC
; TITLE OF INVENTION: ACID SEQUENCING AND SYNTHESIS AND A METHOD OF THEIR
; TITLE OF INVENTION: PREPARATION
; FILE REFERENCE: 2962-109P
; CURRENT APPLICATION NUMBER: US/08/875,243
; CURRENT FILING DATE: 1997-09-16
; EARLIER APPLICATION NUMBER: PCT/SE96/00096

; EARLIER FILING DATE: 1996-01-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-875-243-4

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-875-243-4 (1-20)

QY 32 ValValLysArgArg 36
Db 5 GTGTAAACGACGG 19

RESULT 172
US-09-377-309-45
; Sequence 45, Application US/09377309B
; Patent No. 6258790
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; FILE REFERENCE: ISPH-0390
; CURRENT APPLICATION NUMBER: US/09/377,309B
; CURRENT FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 09/166,203
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-309-45

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-377-309-45 (1-20)

QY 181 LeuProLeuTyrGlu 185
Db 1 TTGCCCTTATATGAG 15

RESULT 173
US-09-377-309-71
; Sequence 71, Application US/09377309B
; Patent No. 6258790
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Condon, Tom P.
; APPLICANT: Cowsett, Lex M.
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
; FILE REFERENCE: ISPH-0390

;; CURRENT APPLICATION NUMBER: US/09/377,309B
;; CURRENT FILING DATE: 1999-08-19
;; EARLIER APPLICATION NUMBER: 09/166,203
;; EARLIER FILING DATE: 1998-10-05
;; NUMBER OF SEQ ID NOS: 99
;; SEQ ID NO 71
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: antisense sequence
US-09-377-309-71

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-377-309-71 (1-20)

QY 181 LeuProLeuTyrGlu 185
DB 4 TTGCCCTTATGAG 18

RESULT 174
US-09-489-869-34/c
; Sequence 34, Application US/09489869A
; Patent No. 6268151
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; APPLICANT: Lex M. Cowsett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE MIGRATION INHIBITORY FACTOR
; FILE REFERENCE: RTS-0110
; CURRENT APPLICATION NUMBER: US/09/489,869A
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-489-869-34

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-489-869-34 (1-20)

QY 125 GlyLeuArgArgLeu 129
DB 17 GGCCTTCGCGGCTC 3

RESULT 175
US-08-750-232-20
; Sequence 20, Application US/08750232
; Patent No. 6270963
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA

;; TITLE OF INVENTION: from a Patient Sample
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson
;; STREET: 1992 Commerce Street, Suite 309
;; CITY: Yorktown Heights
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10598-4412
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS 5.0
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/750,232
;; FILING DATE: 08-JUL-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/271,946
;; FILING DATE: 08-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marina T. Larson
;; REGISTRATION NUMBER: 32,038
;; REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (914) 245-3252
;; TELEFAX: (914) 962-4330
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: genomic DNA
;; HYPOTHETICAL: no
;; ANTI-SENSE: no
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; ORGANISM: human
;; FEATURE:
;; NAME/KEY: primer for exon 21 of human RB1 gene
US-08-750-232-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-750-232-20 (1-20)

QY 28 TyrLeuCyTyrVal 32
DB 2 TACCTATGTTATGTT 16

RESULT 176
US-09-428-583-34
; Sequence 34, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSOLIN-2 EXPRESSION
; FILE REFERENCE: RTS-0096
; CURRENT APPLICATION NUMBER: US/09/428,583
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 34
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-583-34

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-428-583-34 (1-20)

QY 56 HisValGluLeu 60

DB 6 CATGTTGAATTCCTT 20

RESULT 177

; Sequence 64, Application US/09428583
; Patent No. 6271029
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOHESIN-2 EXPRESSION
; FILE REFERENCE: RTS-0096
; CURRENT APPLICATION NUMBER: US/09/428,583
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-428-583-64

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-428-583-64 (1-20)

QY 194 ArgThrLeuGlyLeu 198

DB 3 CGGACATGGGATG 17

RESULT 178

; Sequence 182, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 182
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-593-711A-182

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-593-711A-182 (1-20)

QY 172 LeuSerArgGlnLeu 176

DB 3 CTCGCGGACAGCTG 17

RESULT 179

; Sequence 12, Application US/08682767
; Patent No. 6291741
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of The Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,767
; FILING DATE: 30-July-96
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 51735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-682-767-12

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-12 (1-20)

QY 32 ValVallyArgArg 36

DB 2 GTTGTAACGACGG 16

RESULT 180

; Sequence 16, Application US/08682767
US-08-682-767-16

Patent No. 6291741
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,767
FILING DATE: 30-July-96
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 51735
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-682-767-15

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-16 (1-20)

QY 32 ValVallysArg 36
Db 2 GTGTAAACGACGG 16

RESULT 181
US-08-682-767-18
Sequence 18, Application US/08682767
Patent No. 6291741
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MODIFIED PLANTS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,767

FILING DATE: 30-July-96
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 51735
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-682-767-18

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-682-767-18 (1-20)

QY 32 ValVallysArg 36
Db 2 GTGTAAACGACGG 16

RESULT 182
US-09-484-617-147/c
Sequence 147, Application US/09484617
Patent No. 6303374
GENERAL INFORMATION:
APPLICANT: Hong Zhang
TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
FILE REFERENCE: RIS-0103
CURRENT APPLICATION NUMBER: US/09/484,617
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 147
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-484-617-147

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-484-617-147 (1-20)

QY 41 SerPheSerIeuAsp 45
Db 15 TCCTTCTCCCTGGAC 1

RESULT 183
US-09-721-822A-43
Sequence 43, Application US/09721822A
Patent No. 6306606
GENERAL INFORMATION:
APPLICANT: Michael J. Weber
APPLICATION NUMBER: US/08/682,767


```
; MOLECULE TYPE: CDNA
US-08-750-088A-31

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-750-088A-31 (1-20)

Qy 92 ArgHisValAlaasp 96
Db 4 CGGCATGTCGGAT 18

RESULT 187
US-09-502-344-59
; Sequence 59, Application US/09502344
; Patent No. 6331398
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/502,344
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/143,190
; FILING DATE: August 27, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 nucleotides
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-502-344-59

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-502-344-59 (1-20)

Qy 32 ValValIysArg 36
Db 4 GTTGTAACGACGG 18

RESULT 188
US-09-712-266-67
; Sequence 67, Application US/09712266
; Patent No. 633158
; GENERAL INFORMATION:
; APPLICANT: UEMORI, Takashi
; TITLE OF INVENTION: SATO, Yoshiaki
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUKAI, Hiroyuki
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/712,266
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/446,504
; FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/JP98/02845
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: JP 9-187496
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: JP 9-320692
; PRIOR FILING DATE: 1997-11-27
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

US-09-712-266-67

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-712-266-67 (1-20)

Qy 156 GluArgThrPhelys 160
Db 3 GAGAGAAGCTTCAAG 17

RESULT 189
US-09-658-687A-16
; Sequence 16, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
```

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/09/658,687A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-16

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-658-687A-16 (1-20)

QY 107 ArgIlePheThrAla 111
Db 1 CGTATCTTCACAGCT 15

RESULT 190
US-09-462-261-4
; Sequence 4, Application US/09462261
; Patent No. 6391636
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Oligonucleotide
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jane Massey Licata, Esq.
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: Pentium
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/462,261
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6391636member 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; APPLICATION NUMBER: 08/888,982
; FILING DATE: July 7, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0312
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
```

```
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-462-261-4

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-462-261-4 (1-20)

QY 169 SerValArgLeuSer 173
Db 4 TCTGTAGGCTTCA 18

RESULT 191
US-09-506-073-93
; Sequence 93, Application US/09506073
; Patent No. 6410518
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/506,073
; CURRENT FILING DATE: 2000-02-18
; EARLIER APPLICATION NUMBER: US 09/143,214
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: PCT/US98/13961
; EARLIER FILING DATE: 1998-07-06
; EARLIER APPLICATION NUMBER: US 08/888,982
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US 08/756,806
; EARLIER FILING DATE: 1996-11-26
; EARLIER APPLICATION NUMBER: PCT/US95/07111
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/250,856
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-506-073-93

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-506-073-93 (1-20)

QY 169 SerValArgLeuSer 173
Db 4 TCTGTAGGCTTCA 18

RESULT 192
US-09-907-843-48/c
; Sequence 48, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
```

; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-48

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-907-843-48 (1-20)

Qy 130 HisArgAlaGlyVal 134
Db 20 CACCGGCGAGGTGA 6

RESULT 193

US-09-676-610B-5
; Sequence 5, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-676-610B-5

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-676-610B-5 (1-20)

Qy 129 LeuHisArgAlaGly 133
Db 6 TTGCACAGGCGAGG 20

RESULT 194

US-09-746-694-35
; Sequence 35, Application US/09746694
; Patent No. 6451538
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHK2 EXPRESSION
; FILE REFERENCE: RTS-0228
; CURRENT APPLICATION NUMBER: US/09/746,694
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 35
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-746-694-35

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-746-694-35 (1-20)

Qy 110 ThrAlaArgLeuTyr 114
Db 4 ACAGCAGGTTATAC 18

RESULT 195

US-09-920-672-58
; Sequence 58, Application US/09920672
; Patent No. 6455308
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/920,672
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-672-58

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-920-672-58 (1-20)

Qy 42 PheSerLeuAspPhe 46
Db 3 TTCTCGTTGGACTTC 17

RESULT 196

US-09-657-453A-71/C
; Sequence 71, Application US/09657453A
; Patent No. 6458591
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 2 EXPRESSION
; FILE REFERENCE: RTS-0136
; CURRENT APPLICATION NUMBER: US/09/657,453A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 105
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-453A-71

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-657-453A-71 (1-20)

Qy 38 SerAlaThrSerPhe 42

Db 15 TCTGCCACTTCTTTT 1

RESULT 197

US-09-153-242-56

; Sequence 56, Application US/09153242

; Patent No. 6482592

; GENERAL INFORMATION:

; APPLICANT: Lundberg, Joakim

; APPLICANT: Uhlen, Mathias

; TITLE OF INVENTION: MODULAR PROBES II

; FILE REFERENCE: 1181-242

; CURRENT APPLICATION NUMBER: US/09/153,242

; CURRENT FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: PCT/GB97/02629

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 56

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: KTH USP

US-09-153-242-56

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-153-242-56 (1-20)

Qy 32 ValValLysArgArg 36

Db 2 GTTGTAAACGACGG 16

RESULT 198

US-09-668-313A-78/c

; Sequence 78, Application US/09668313A

; Patent No. 6503756

; GENERAL INFORMATION:

; APPLICANT: Brett P. Morita

; APPLICANT: Susan M. Freier

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION

; FILE REFERENCE: RTS-0127

; CURRENT APPLICATION NUMBER: US/09/668,313A

; CURRENT FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 247

; SEQ ID NO 78

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-668-313A-78

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-668-313A-78 (1-20)

Qy 44 LeuAspPheGlyTyr 48

Db 17 CTGGACTTTGGGTAT 3

RESULT 199

US-09-198-452A-3206/c

; Sequence 3206, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Grifffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3206

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3206

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-3206 (1-20)

Qy 169 SerValArgLeuSer 173

Db 19 TCCGTGAGACTGTCT 5

RESULT 200

US-09-198-452A-3704/c

; Sequence 3704, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Grifffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3704

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3704

Alignment Scores:

Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-3704 (1-20)

Qy 103 AsnLeuSerLeuArg 107
Db 20 AACCTCTCTGTGAGG 6

RESULT 201

US-09-198-452A-3731/C

; Sequence 3731, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3731

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3731

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-3731 (1-20)

Qy 104 LeuSerLeuArgIle 108

Db 16 TTGTCTCTGGAATC 2

RESULT 202

US-09-198-452A-3975

; Sequence 3975, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 3975

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3975

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-3975 (1-20)

Qy 176 LeuArgIleLeu 180

Db 6 TTGAGGAGGATCTGT 20

RESULT 203

US-09-198-452A-4543

; Sequence 4543, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4543

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4543

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-4543 (1-20)

Qy 111 AlaArgLeuTyrPhe 115

Db 2 GCCAGGCTGTATTC 16

RESULT 204

US-09-198-452A-4632/C

; Sequence 4632, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4632

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4632

Alignment Scores:

Pred. No.:	1.11e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-198-452A-4632 (1-20)

Qy 179 IleLeuLeuProLeu 183

Db 20 ATTCTACTCCCTCTC 6

RESULT 205

US-09-198-452A-4660/C

; Sequence 4660, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

```
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4660
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4660

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-4660 (1-20)
QY 40 ThrSerPheSerLeu 44
DB 18 ACATCGTCTCCCTA 4

RESULT 206
US-09-198-452A-5412/c
; Sequence 5412, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5412
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5412

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-5412 (1-20)
QY 126 LeuArgArgLeuHis 130
DB 17 CTAAGCGCTTACAT 3

RESULT 207
US-09-198-452A-5709/c
; Sequence 5709, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5709
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5709

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-5709 (1-20)
QY 104 LeuSerLeuArgIle 108
DB 15 CTGCTCTCCGCATA 1

RESULT 208
US-09-198-452A-6382/c
; Sequence 6382, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6382
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6382

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-6382 (1-20)
QY 58 GluLeuLeuPheLeu 62
DB 20 GAGCTTCTCTTTTA 6

RESULT 209
US-09-198-452A-6501
; Sequence 6501, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6501

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
```

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-198-452A-6501 (1-20)

QY 41 SerPheSerLeuAsp 45
DB 5 AGTTTCTCTAGAC 19

RESULT 210

US-09-843-376-54
; Sequence 54, Application US/09843376
; Patent No. 6586132
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 1 EXPRESSION
; FILE REFERENCE: RTS-0234
; CURRENT APPLICATION NUMBER: US/09/843,376
; CURRENT FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-843-376-54

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-843-376-54 (1-20)

QY 167 GluAsnSerValArg 171
DB 5 GAGATTTCAGTGAGG 19

RESULT 211

US-09-909-595-70/c
; Sequence 70, Application US/09909595
; Patent No. 6586245
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Brenda F. Baker
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Scott E. Davis
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
; FILE REFERENCE: RTS-0223
; CURRENT APPLICATION NUMBER: US/09/909,595
; CURRENT FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-70

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-909-595-70 (1-20)

QY 2 AspSerLeuMet 6
DB 15 GACAGTCTTCTCATG 1

RESULT 212

US-09-972-115A-26
; Sequence 26, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-972-115A-26

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-972-115A-26 (1-20)

QY 25 ArgGluThrTyrLeu 29
DB 5 CGAGAGACTTATCTC 19

RESULT 213

US-09-276-438-16
; Sequence 16, Application US/09276438
; Patent No. 6600027
; GENERAL INFORMATION:
; APPLICANT: Krishnan, Rajendra
; APPLICANT: Coleman, Rebecca A.
; APPLICANT: Yoder, Christine C.
; APPLICANT: Durtschi, Becky A.
; APPLICANT: Brake, David
; TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULES ENCODING NEOSPORA PROTEINS
; FILE REFERENCE: PC9943A
; CURRENT APPLICATION NUMBER: US/09/276,438
; CURRENT FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: 60/079,389
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 60/112,282
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.0 - beta
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA


```
/
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
/ STREET: 1420 Fifth Avenue
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101-8100
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/10261A
/ FILING DATE: 02-SEP-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Shelton, Dennis K.
/ REGISTRATION NUMBER: 26,997
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 682-8100
/ TELEFAX: (206) 224-0779
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ DESCRIPTION: PCR primer; see TABLE 1
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ PCT-US94-10261A-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-10261A-20 (1-20)

Cy 59 LeuLeuPheLeuArg 63
Db 19 TTGCTATTCTCAGA 5

RESULT 218
PCT-US95-08604-20
; Sequence 20, Application PC/TUS9508604
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: HSC Research and Development Limited Partnership
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
/
```

```
/
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/08604
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION NUMBER: US 08/271,942
/ FILING DATE: 08-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marina T. Larson
/ REGISTRATION NUMBER: 32,038
/ REFERENCE/DOCKET NUMBER: VGEN.P-003-WO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (914) 245-3252
/ TELEFAX: (914) 962-4330
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: human
/ FEATURE:
/ NAME/KEY: primer for exon 21 of human RB1 gene
/ PCT-US95-08604-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US95-08604-20 (1-20)

Cy 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16

RESULT 219
PCT-US95-08606-20
; Sequence 20, Application PC/TUS9508606
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Stevens, John K.
; APPLICANT: Dunn, James M.
; APPLICANT: Capatos, Denis
; APPLICANT: Matthews, David E.
; TITLE OF INVENTION: Method for Testing for Mutations in DNA
; TITLE OF INVENTION: from a Patient Sample
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
/
```

```
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA: US 08/271,946
/ APPLICATION NUMBER: 08-JUL-1994
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marina T. Larson
/ REGISTRATION NUMBER: 32,038
/ REFERENCE/DOCKET NUMBER: VGEN.P-002-WO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (914) 245-3252
/ TELEFAX: (914) 962-4330
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: human
/ FEATURE:
/ NAME/KEY: primer for exon 21 of human Rb1 gene
/ PCT-US95-08606-20

Alignment Scores:
Pred. No.: 1.11e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.53%
Indels: 0
Gaps: 0
DB: 0

US-09-966-880A-8 (1-198) x PCT-US95-08606-20 (1-20)

QY 28 TyrLeuCysTyrVal 32
Db 2 TACCTATGTTATGTT 16

RESULT 220
US-07-974-447-16
/ Sequence 16, Application US/07974447
/ Patent No. 5436142
/ GENERAL INFORMATION:
/ APPLICANT: Wigler, Michael H
/ APPLICANT: Libitsyn, Nikolai
/ TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO GENOMIC
/ TITLE OF INVENTION: ANALYSIS
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/974,447
/ FILING DATE: 12-NOV-1992
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20,015
/ REFERENCE/DOCKET NUMBER: A-57438/BIR CSHL-002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 3983249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-149-199-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00%
Conservative: 0
```

```
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-07-974-447-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 1

US-09-966-880A-8 (1-198) x US-07-974-447-16 (1-12)

QY 41 SerPheSerLeu 44
Db 1 AGCTTCTCCCTC 12

RESULT 221
US-08-149-199-16
/ Sequence 16, Application US/08149199
/ Patent No. 5501964
/ GENERAL INFORMATION:
/ APPLICANT: Wigler, Michael H
/ APPLICANT: Libitsyn, Nikolai
/ TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO GENOMIC
/ TITLE OF INVENTION: ANALYSIS
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
/ STREET: 4 Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 941114187
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MSDOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/149,199
/ FILING DATE: 9-No. 5501964-93
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20,015
/ REFERENCE/DOCKET NUMBER: A57438/BIR CSHL002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 7811989
/ TELEFAX: (415) 3983249
/ TELEX: 910 277299
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-149-199-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00%
Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DBs: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-149-199-16 (1-12)

QY 41 SerpheSerLeu 44
Db 1 AGCTTCTCCCTC 12

RESULT 222
US-08-757-024-852/c
; Sequence 852, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 852:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-852

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DBs: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-852 (1-12)

QY 90 CysalaArgHis 93
Db 12 TGTGCCCGCCAT 1

RESULT 223
US-09-115-061-16
; Sequence 16, Application US/09115061A
; Patent No. 6159713
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael
; APPLICANT: Listitsyn, Nikolai
; TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS

; FILE REFERENCE: CSHL.002.03US
; CURRENT APPLICATION NUMBER: US/09/115,061A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 08/478,242
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/149,199
; EARLIER FILING DATE: 1993-11-09
; EARLIER APPLICATION NUMBER: 07/974,447
; EARLIER FILING DATE: 1992-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-115-061-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DBs: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-115-061-16 (1-12)

QY 41 SerpheSerLeu 44
Db 1 AGCTTCTCCCTC 12

RESULT 224
US-09-049-190-15/c
; Sequence 15, Application US/09049190
; Patent No. 6190866
; GENERAL INFORMATION:
; APPLICANT: Nielsen et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having
; TITLE OF INVENTION: Antibacterial Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,190
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 bases
; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-lysine-glycine
; OTHER INFORMATION: backbone
; US-09-049-190-15

```

```

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-049-190-15 (1-12)

```

```

Qy 119 ArgLysAlaGlu 122
Db 12 AGAAGGCAGAA 1

RESULT 225
US-08-098-327E-39/c
; Sequence 39, Application US/08098327E
; Patent No. 6270771
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,327E
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; US-08-098-327E-39

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-098-327E-39 (1-12)

Qy 59 LeuLeuPheLeu 62
Db 12 TTGTTGTTCTTG 1

RESULT 226
US-08-098-327E-43/c
; Sequence 43, Application US/08098327E
; Patent No. 6270771
; GENERAL INFORMATION:

```



```

; APPLICANT: GUERIN-MARCHAND, Claudine
; APPLICANT: DRUILHE, Pierre
; TITLE OF INVENTION: PETIDE SEQUENCES SPECIFIC FOR THE
; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098,327E
; FILING DATE: 24-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; US-08-098-327E-43

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-098-327E-43 (1-12)
QY 59 LeuLeuPheLeu 62
Db 12 TTGTTGTTCTTG 1

RESULT 227
US-09-261-079-16
; Sequence 16, Application US/09261079
; Patent No. 6277606
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael
; APPLICANT: Lisitsyn, Nikolai
; TITLE OF INVENTION: A REPRESENTATIONAL APPROACH TO DNA ANALYSIS
; FILE REFERENCE: CSHL.002.04US
; CURRENT APPLICATION NUMBER: US/09/261,079
; CURRENT FILING DATE: 1999-03-02
; EARLIER APPLICATION NUMBER: 08/478,242
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 07/974,447
; EARLIER FILING DATE: 1992-11-12

```

```

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; TYPE: DNA
; LENGTH: 12
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: OLIGONUCLEOTIDE
US-09-261-079-16

Alignment Scores:
Pred. No.: 7.75e+03 Length: 12
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-261-079-16 (1-12)
QY 41 SerPheSerLeu 44
Db 1 AGCTTCTCCCTC 12

RESULT 228
US-08-932-140C-15/c
; Sequence 15, Application US/08932140C
; Patent No. 6300318
; GENERAL INFORMATION:
; APPLICANT: Nielsen et al.
; TITLE OF INVENTION: Peptide Nucleic Acids Having
; TITLE OF INVENTION: Antibacterial Activity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6300318ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/932,140C
; FILING DATE: September 16, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-2560
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: N-acetyl (2-aminoethyl)glycine
; OTHER INFORMATION: backbone
; FEATURE:

```

NAME/KEY: Modified-site
 LOCATION: 2
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 3
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 9
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 11
 OTHER INFORMATION: N-acetyl(2-aminoethyl)glycine
 OTHER INFORMATION: backbone
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: N-[acetyl(2-aminoethyl)]-C-
 OTHER INFORMATION: lysine-glycine backbone
 US-08-932-140C-15

Alignment Scores:
 Pred. No.: 7.75e+03 Length: 12
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-932-140C-15 (1-12)

QY 119 ArgIysAlaGlu 122
 DB 12 AGAAGGCAGAA 1

RESULT 229

US-08-462-625-39/c

; Sequence 39, Application US/08462625

; Patent No. 6319502
 ; GENERAL INFORMATION:
 ; APPLICANT: GUERIN-MARCHAND, Claudine
 ; APPLICANT: DRUILHE, Pierre
 ; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
 ; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
 ; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,625
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/038,327
 ; FILING DATE: 24-NOV-1993
 ; PRIOR APPLICATION DATA: FR 91 01286
 ; FILING DATE: 05-FEB-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm K.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 010830-078
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; PUBLICATION INFORMATION:
 ; DOCUMENT NUMBER: WO 92/13884
 ; PUBLICATION DATE: 20-AUG-1992
 ; US-08-462-625-39

Alignment Scores:
 Pred. No.: 7.75e+03 Length: 12
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-462-625-39 (1-12)

QY 59 LeuLeuPheLeu 62
 DB 12 TTGTTGTTCTTG 1

RESULT 230

US-08-462-625-43/c

; Sequence 43, Application US/08462625

; Patent No. 6319502

; GENERAL INFORMATION:

; APPLICANT: GUERIN-MARCHAND, Claudine

; APPLICANT: DRUILHE, Pierre

; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE

; TITLE OF INVENTION: HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE

; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES

```

; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,625
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/098,327
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 92/13884
; PUBLICATION DATE: 20-AUG-1992
; US-08-462-625-43
;
; Alignment Scores:
; Pred. No.: 7.75e+03 Length: 12
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 4 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-462-625-43 (1-12)
;
; QY 59 LeuLeuPheLeu 62
; Db 12 TTGTTGTTCTTG 1
;
; RESULT 231
; US-08-173-489C-350/c
; Sequence 350, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 350:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from p53 gene
; DESCRIPTION: region in Seq ID No. 5861244349
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 350 :FROM 1 TO 13
; US-08-173-489C-350
;
; Alignment Scores:
; Pred. No.: 8.38e+03 Length: 13
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 2 Gaps: 0
;
; US-09-966-880A-8 (1-198) x US-08-173-489C-350 (1-13)
;
; QY 22 LysGlyArgArg 25
; Db 13 AAAGAAGGCGA 2
;
; RESULT 232
; US-08-757-024-840/c
; Sequence 840, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 840:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-840

Alignment Scores:
Pred. No.: 8.38e+03 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-840 (1-13)

Qy 90 CysalaargHis 93
Db 13 TGTGCCCGCAT 2

RESULT 233
US-08-757-024-851/c
; Sequence 851, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 851:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-851

Alignment Scores:
Pred. No.: 8.38e+03 Length: 13

```

```

Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-851 (1-13)

Qy 90 CysalaargHis 93
Db 12 TGTGCCCGCAT 1

RESULT 234
US-08-981-988A-39/c
; Sequence 39, Application US/08981988A
; Patent No. 6337194
; GENERAL INFORMATION:
; APPLICANT: Vittal Mallya Scientific Research Foundation
; APPLICANT: The University of Leicester
; TITLE OF INVENTION: Insulin
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: VITTAL MALLYA SCIENTIFIC RESEARCH FOUNDATION
; STREET: K. R. ROAD
; CITY: BANGALORE
; COUNTRY: INDIA
; ZIP: 560 004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,988A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513967.1
; FILING DATE: 08-JUL-1995
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-981-988A-39

Alignment Scores:
Pred. No.: 8.38e+03 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-981-988A-39 (1-13)

Qy 41 SerPheSerLeu 44
Db 12 AGCTTCAGCCTC 1

RESULT 235
US-08-532-657A-3/c
; Sequence 3, Application US/08532657A
; Patent No. 6346414
; GENERAL INFORMATION:
; APPLICANT: JACOBS, Eric
; TITLE OF INVENTION: TRANSPOSITION ASSEMBLY FOR GENE TRANSFER
; TITLE OF INVENTION: IN EUKARYOTES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404

```

CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,657A
FILING DATE: 16-OCT-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00419
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/04530
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 017753-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: synthetic oligonucleotide
US-08-532-657A-3

Alignment Scores:
Pred. No.: 13
Score: 8.38e+03
Length: 13
Matches: 4
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-532-657A-3 (1-13)

Qy 46 PheGlyTyrLeu 49
| | | | | | | | | | | | |
Db 13 TTTCGTACCTT 2

RESULT 236
US-09-323-872A-58/c
; Sequence 58, Application US/09323872A
; Patent No. 6395539
; GENERAL INFORMATION:
; APPLICANT: Coschigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-01640
; CURRENT APPLICATION NUMBER: US/09/323,872A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-323-872A-58

Alignment Scores:
Pred. No.: 13
Score: 8.38e+03
Length: 13
Matches: 4
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-09-323-872A-58 (1-13)

Qy 195 ThrLeuGlyLeu 198
| | | | | | | | | | | | |
Db 13 ACACGAGGCTG 2

RESULT 237
US-08-275-951-65
; Sequence 65, Application US/08275951
; Patent No. 6451968
; GENERAL INFORMATION:
; APPLICANT: Egholm, Michael
; APPLICANT: Kiely, John
; APPLICANT: Griffin, Michael
; APPLICANT: Coull, James M.
; APPLICANT: Neilsen, Peter
; APPLICANT: Buchardt, Ole
; APPLICANT: Dueholm, Kim L.
; APPLICANT: Christensen, Leif
; TITLE OF INVENTION: Linked Peptide Nucleic Acids
; FILE REFERENCE: ISIS1577
; CURRENT APPLICATION NUMBER: US/08/275,951
; CURRENT FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/108,591
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: 08/088,658
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: 08/088,661
; PRIOR FILING DATE: 1993-07-02
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: 986/91
; PRIOR FILING DATE: 1991-05-22
; PRIOR APPLICATION NUMBER: 987/91
; PRIOR FILING DATE: 1991-05-24
; PRIOR APPLICATION NUMBER: 510/92
; PRIOR FILING DATE: 1991-04-15
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
US-08-275-951-65

Alignment Scores:
Pred. No.: 13
Score: 8.38e+03
Length: 13
Matches: 4
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0

US-09-966-880A-8 (1-198) x US-08-275-951-65 (1-13)

Qy 24 ArgArgGluThr 27
| | | | | | | | | | | | |
Db 1 CGCAGAGAACG 12

RESULT 238
US-09-216-584-1
; Sequence 1, Application US/09216584
; Patent No. 6548657

```

; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bellon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-1

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0
Gaps:           4            0

US-09-966-880A-8 (1-198) x US-09-216-584-1 (1-13)

Qy 59 LeuLeupheLeu 62
   |||||
Db 1 TTGCTTTTCCTC 12

RESULT 239
US-09-216-584-2
; Sequence 2, Application US/09216584
; Patent No. 6548657
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bellon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-2

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0
Gaps:           4            0

```

```

Query Match:    2.02%        0
DB:             4            0
Gaps:           4            0

US-09-966-880A-8 (1-198) x US-09-216-584-2 (1-13)

Qy 59 LeuLeupheLeu 62
   |||||
Db 2 TTGCTTTTCCTC 13

RESULT 240
US-09-216-584-13
; Sequence 13, Application US/09216584
; Patent No. 6548657
; GENERAL INFORMATION:
; APPLICANT: Alex, Burgin
; APPLICANT: Leonid, Beigelman
; APPLICANT: Laurent, Bellon
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBH00-853-A; RPI 237/167
; CURRENT APPLICATION NUMBER: US/09/216,584
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Accessible site within Bcl-2 transcript
US-09-216-584-13

Alignment Scores:
Pred. No.:      8.38e+03      13
Score:          4.00         4
Percent Similarity: 100.00%   0
Best Local Similarity: 100.00% 0
Query Match:    2.02%        0
DB:             4            0
Gaps:           4            0

US-09-966-880A-8 (1-198) x US-09-216-584-13 (1-13)

Qy 70 LeuAspProGly 73
   |||||
Db 1 CTGGATCCAGGA 12

RESULT 241
US-09-083-235A-74
; Sequence 74, Application US/09083235A
; Patent No. 6632919
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E
; APPLICANT: Haalma, Gerald
; APPLICANT: Eldrup, Anne B
; TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
; FILE REFERENCE: ISIS3044
; CURRENT APPLICATION NUMBER: US/09/083,235A
; CURRENT FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 08/862,629
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 74
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-74

Alignment Scores:
Pred. No.: 8.38e+03 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-083-235A-74 (1-13)

Qy 24 ArgArgGluThr 27
Db 1 CGCAGAGAACG 12

RESULT 242
US-09-083-235A-78
Sequence 78, Application US/09083235A
Patent No. 6632919
GENERAL INFORMATION:
APPLICANT: Nielsen, Peter E
APPLICANT: Haaima, Gerald
APPLICANT: Eldrup, Anne B
TITLE OF INVENTION: Peptide Nucleic Acid Monomers and Oligomers
FILE REFERENCE: ISIS3044
CURRENT APPLICATION NUMBER: US/09/083,235A
CURRENT FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 08/862,629
PRIOR FILING DATE: 1997-05-23
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 78
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6632919el Sequence
US-09-083-235A-78

Alignment Scores:
Pred. No.: 8.38e+03 Length: 13
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-083-235A-78 (1-13)

Qy 24 ArgArgGluThr 27
Db 1 CGCAGAGAACG 12

RESULT 243
US-08-375-116A-122/c
Sequence 122, Application US/08375116A
Patent No. 5631146
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Huizenga, David E.
TITLE OF INVENTION: DNA APIMERs AND CATALYSTS THAT BIND
TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE-5'-PHOSPHATES AND METHODS FOR
ISOLATION THEREOF
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,116A
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/266001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (9617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-375-116A-122

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-375-116A-122 (1-14)

Qy 61 PheLeuArgTyr 64
Db 12 TTCCTCCGCTAT 1

RESULT 244
US-08-320-559-16/c
Sequence 16, Application US/08320559
Patent No. 5633135
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Ganaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/888,830
;; FILING DATE: 27-MAY-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/805,093
;; FILING DATE: 11-DEC-91
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-0855
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: No
US-08-320-559-16

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-320-559-16 (1-14)

QY 46 PheGlyTyrLeu 49
DB 13 TTITGGGTACCT 2

RESULT 245

;; Sequence 16, Application US/08327392
;; Patent No. 5633136
;; GENERAL INFORMATION:
;; APPLICANT: Croce, Carlo
;; APPLICANT: Canaan, Eli
;; TITLE OF INVENTION: ALL-1 Polynucleotides and Monoclonal
;; TITLE OF INVENTION: Antibodies for Leukemia Detection and
;; TITLE OF INVENTION: Treatment
;; NUMBER OF SEQUENCES: 24
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633136ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/327,392
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/971,094
;; FILING DATE: 30-OCT-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/888,830
;; FILING DATE: 27-MAY-92
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/805,093
;; FILING DATE: 11-DEC-91
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Deluca, Mark
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: TJU-1331
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: No
US-08-327-392-16

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-327-392-16 (1-14)

QY 46 PheGlyTyrLeu 49
DB 13 TTITGGGTACCT 2

RESULT 246

;; US-08-486-421-42
;; Sequence 42, Application US/08486421
;; Patent No. 5672479
;; GENERAL INFORMATION:
;; APPLICANT: Johnson, Edward M.
;; APPLICANT: Bergemann, Andrew D.
;; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
;; NUMBER OF SEQUENCES: 51
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,421
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470,911
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 6923-053
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 42:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-486-421-42

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-485-421-42 (1-14)

Qy 126 LeuArgArgLeu 129
Db 3 CTTCGCCGCC 14

RESULT 247

US-08-135-809A-5/c
; Sequence 5, Application US/08135809A
; Patent No. 5688677

GENERAL INFORMATION:
; APPLICANT: CHENG, SENG H.
; APPLICANT: DITULLIO, PAUL
; APPLICANT: EBERT, KARL M.
; APPLICANT: MEADE, HARRY M.
; APPLICANT: SMITH, ALAN E.
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: INACTIVATED HORMONE RESPONSIVE ELEMENTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/135,809A
; FILING DATE: 13-OCT-1993

CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: IG4-9.12

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415

INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: cDNA
US-08-135-809A-5

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-135-809A-5 (1-14)

Qy 2 AppSerLeuLeu 5
Db 12 GACAGCCTCTC 1

RESULT 248

US-08-271-880A-210/c
; Sequence 210, Application US/08271880A
; Patent No. 5693535

GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,880A
; FILING DATE: July 7, 1994

PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993

APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-271-880A-210

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-271-880A-210 (1-14)

Qy 10 LysPheLeuTyr 13
Db 12 AAGTTCTCTAT 1

RESULT 249

US-08-271-880A-211/c
; Sequence 211, Application US/08271880A
; Patent No. 5693535

```

; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,880A
; FILING DATE: July 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-271-880A-211
; Alignment Scores:
; Pred. No.: 9.02e+03 Length: 14
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 1 Gaps: 0
; US-09-966-880A-8 (1-198) x US-08-271-880A-211 (1-14)
;
; Qy 11 PheLeuTyxGln 14
; Db 12 TTTCCTCATCAA 1
;
; RESULT 250
; US-08-470-911-42
; Sequence 42, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-470-911-42
; Alignment Scores:
; Pred. No.: 9.02e+03 Length: 14
; Score: 4.00 Matches: 4
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 2.02% Indels: 0
; DB: 1 Gaps: 0
; US-09-966-880A-8 (1-198) x US-08-470-911-42 (1-14)
;
; Qy 126 LeuArgArgLeu 129
; Db 3 CTTCGGCGCTC 14
;
; RESULT 251
; US-08-323-192D-66/c
; Sequence 66, Application US/08323192D
; Patent No. 5785199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

```
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-323-192D-66

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-323-192D-66 (1-14)

Qy 59 LeuLeuPheLeu 62
Db 14 CTCCTGTCTCTA 3

RESULT 252
US-08-470-887A-54/c
Sequence 54, Application US/08470887A
Patent No. 5820871
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,887A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA
US-08-470-887A-54

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-470-887A-54 (1-14)

Qy 59 LeuLeuPheLeu 62
Db 14 CTCCTGTCTCTA 3

RESULT 254
US-08-486-809-42
```

```
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-323-192D-66

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-470-887A-54 (1-14)

Qy 59 LeuLeuPheLeu 62
Db 14 CTCCTGTCTCTA 3

RESULT 253
US-08-252-508B-54/c
Sequence 54, Application US/08252508B
Patent No. 5854037
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,508B
FILING DATE: 01-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: RNA
US-08-252-508B-54

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-252-508B-54 (1-14)

Qy 59 LeuLeuPheLeu 62
Db 14 CTCCTGTCTCTA 3

RESULT 254
US-08-486-809-42
```

; Sequence 42, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-486-809-42

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-486-809-42 (1-14)

Qy 126 LeuArgLeu 129
Db 3 CTTGCGCGCTC 14

RESULT 255
US-08-910-408-210/c
; Sequence 210, Application US/08910408
; Patent No. 5972704
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/910,408
; APPLICATION NUMBER: US/08/910,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,880
; FILING DATE: July 7, 1994
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-910-408-210

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-910-408-210 (1-14)

Qy 10 LysPheLeuTyr 13
Db 12 AAGTTTCTCTAT 1

RESULT 256
US-08-910-408-211/c
; Sequence 211, Application US/08910408
; Patent No. 5972704
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

```

; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,880
; FILING DATE: July 7, 1994
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-910-408-211

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) X US-08-910-408-211 (1-14)

Qy 11 PheLeuTyrgln 14
Db 12 TTTCCTATCAA 1

RESULT 257
US-08-520-933-4
; Sequence 4, Application US/08520933
; Patent No. 5981194
; GENERAL INFORMATION:
; APPLICANT: Jefferies, Wilfred A.
; APPLICANT: McGeer, Patrick L.
; APPLICANT: Rothernberger, Sylvia
; APPLICANT: Food, Michael R.
; APPLICANT: Yamada, Tatsuo
; APPLICANT: Kennard, Malcolm
; TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
; TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,933
; FILING DATE: August 31, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Shona S. McDiarmid
; REGISTRATION NUMBER: 38,798
; REFERENCE/DOCKET NUMBER: 7685-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-364-7311
; TELEFAX: 416-361-1398
; TELEX: 06-23115
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-520-933-4

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) X US-08-520-933-4 (1-14)

Qy 95 AlaAspPheLeu 98
Db 1 GCGGACTTCCTC 12

RESULT 258
US-09-106-377-54/c
; Sequence 54, Application US/09106377
; Patent No. 6001634
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,377
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/252,508
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7692-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

```

; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA
US-09-106-377-54

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-106-377-54 (1-14)

Oy 59 LeuLeupheLeu 62
Db 14 CTCCTGTTCTCA 3

RESULT 259
US-08-757-024-827/c
; Sequence 827, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 827:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-827

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-08-757-024-827
; Sequence 827, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-827 (1-14)

Oy 90 CysAlaArgHis 93
Db 14 TGTGCCGCCAT 3
RESULT 260
US-08-757-024-839/c
; Sequence 839, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,024
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 839:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-024-839

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-839 (1-14)

Oy 90 CysAlaArgHis 93
Db 13 TGTGCCGCCAT 2

RESULT 261
US-08-757-024-850/c
; Sequence 850, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina

```

; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 850:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-024-850

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-757-024-850 (1-14)

Qy 90 CysAlaArgHis 93
Db 12 TTGTCCCGCAT 1

RESULT 262
US-08-545-860D-16/c
; Sequence 16, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: No
; US-08-545-860D-16

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-545-860D-16 (1-14)

Qy 46 PheGlyTyrLeu 49
Db 13 TTGGGTACCTT 2

RESULT 263
US-08-985-162-1779/c
; Sequence 1779, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1779:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-1779

```

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Alignment Scores:
Pred. No.: 14
Score: 9.02e+03
Length: 14
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 0

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US-09-966-880A-8 (1-198) x US-08-985-162-1779 (1-14)

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Qy 130 HisaGAlagly 133
Db 13 CACAGGCGGG 2

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RESULT 264

```

; Sequence 1821, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-1821

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Alignment Scores:
Pred. No.: 9.02e+03
Score: 4.00
Length: 14
Matches: 4
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 2.02%
Indels: 0
Gaps: 0
DB: 0

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US-09-966-880A-8 (1-198) x US-08-985-162-1821 (1-14)

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Qy 134 ValGlnIleAla 137
Db 1 GUGCAGAUCCGA 12

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RESULT 265

```

; US-09-249-215-210/c
; Sequence 210, Application US/09249215
; Patent No. 6159692
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowrira
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,215
; FILING DATE: 12-Feb-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,408
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard

```



```
;
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-09-249-215-210
Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-249-215-210 (1-14)
QY 10 LysPheLeuTyr 13
Db 12 AAGTTCTCTAT 1
RESULT 266
US-09-249-215-211/c
; Sequence 211, Application US/09249215
; Patent No. 6159692
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; Bharat Chowrira
; James McSwiggen
; Dan T. Stinchcomb
; James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; HUMAN IMMUNODEFICIENCY VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,215
; FILING DATE: 12-Feb-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,408
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
```

```
;
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-249-215-211
Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-249-215-211 (1-14)
QY 11 PheLeuTyrGln 14
Db 12 TTTCTCTATCAA 1
RESULT 267
US-09-156-828B-25/c
; Sequence 25, Application US/09156828B
; Patent No. 6238217
; GENERAL INFORMATION:
; APPLICANT: Hendry, Philip
; APPLICANT: McCall, Maxine J.
; TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZYMES
; FILE REFERENCE: 50534bpu
; CURRENT APPLICATION NUMBER: US/09/156,828B
; CURRENT FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PCT/AU97/00210
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and Portions their
US-09-156-828B-25
Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 3 Gaps: 0
US-09-966-880A-8 (1-198) x US-09-156-828B-25 (1-14)
QY 95 AlaAspPheLeu 98
Db 14 GCTGACTTCTGT 3
RESULT 268
US-08-666-341A-75
; Sequence 75, Application US/08666341A
; Patent No. 6365345
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antisense nucleic Acids for the
; prevention and treatment of disorders in which expression
; of c-erbB plays a role
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Jacobson, Price, Holman and Stern, PLLC
STREET: 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,341A
FILING DATE: 15-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93120710.4
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-666-341A-75

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-666-341A-75 (1-14)

QY 172 LeuSexArgGln 175
|||||
Db 1 CTGTCGTCTCAA 12

RESULT 269
US-09-285-040-4
Sequence 4, Application US/09285040
Patent No. 6455494
GENERAL INFORMATION:
APPLICANT: Jefferies, Wilfred A.
APPLICANT: McGeer, Patrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Food, Michael R.
APPLICANT: Yamada, Tatsuo
APPLICANT: Kennard, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereekin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,040
FILING DATE: 01-APR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline

REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7695-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-285-040-4

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-285-040-4 (1-14)

QY 95 AlaAspPheLeu 98
|||||
Db 1 GCGGACTTCCTC 12

RESULT 270
US-09-516-277-14
Sequence 14, Application US/09516277
Patent No. 6528701
GENERAL INFORMATION:
APPLICANT: WANG -- OARD
TITLE OF INVENTION: RICE UBQUITIN-DERIVED PROMOTERS
FILE REFERENCE: 98A5
CURRENT APPLICATION NUMBER: US/09/516,277
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 14
TYPE: DNA
ORGANISM: Zea mays
US-09-516-277-14

Alignment Scores:
Pred. No.: 9.02e+03 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-516-277-14 (1-14)

QY 36 ArgAspSerAla 39
|||||
Db 3 CGAGATTCGCT 14

RESULT 271
US-08-192-943-14/C
Sequence 14, Application US/08192943
Patent No. 6544755
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
TITLE OF INVENTION: BY EXPRESSION OF THE c-MYC
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 41